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ISOFORMS OF STARCH BRANCHING ENZYME II (SBE-IIA AND SBE-IIB) FROM WHEAT

Field of the Invention

This invention relates generally to plant starch compositions, and concerns novel nucleotide sequences; polypeptides encoded thereby; vectors and host cells and host organisms comprising one or more of the novel sequences; a method of altering one or more characteristics of a plant; a plant having altered characteristics; starch obtained from such plants; and uses of the starch.

Background to the Invention

The majority of developments in cereal science in the recent past have concentrated primarily on the functionality of the gluten protein sub-units and their role in bakery systems. This has been greatly facilitated by the abundance of natural variation between cultivators for the gluten protein sub-unit components.

In contrast, although flour from commercially grown wheat varieties contains approximately 75-85% starch, the role of starch from a breeding perspective has been overlooked; this is largely due to the difficulty of measuring differences in starch structure. Of the limited amount of work that has been carried out however, there appears to be a lack of natural variation between different wheat cultivars. With the advent of recombinant DNA and gene transfer technologies it is now possible to create new variation *in planta*, therefore directly modifying starch composition in wheat becomes a realistic target.

Starch is the major form of carbon reserve in plants, constituting 50% or more of the dry weight of many storage organs, e.g. tubers, seeds of cereals. Starch is used in numerous food and industrial applications. In many cases, however, it is necessary to modify the native starches, via chemical or physical means, in order to produce distinct properties to

suit particular applications. It would be highly desirable to be able to produce starches with the required properties directly in the plant, thereby removing the need for additional modification. To achieve this via genetic engineering requires knowledge of the metabolic pathway of starch biosynthesis. This includes characterisation of genes and encoded gene products which catalyse the synthesis of starch. Knowledge about the regulation of starch biosynthesis raises the possibility of "re-programming" biosynthetic pathways to create starches with novel properties that could have new commercial applications.

The most significant property of starch derives from the ability of the native granular form to lose its order and to swell and absorb water upon suitable treatment, thereby conferring viscosity and texture, in a process known as gelatinisation. Gelatinisation has been defined (W A Atwell *et al*, 1988) as "... the collapse (disruption) of molecular orders within the starch granule manifested in irreversible changes in properties such as granular swelling, native crystallite melting, loss of birefringence, and starch solubilisation. The point of initial gelatinisation and the range over which it occurs is governed by starch concentration, method of observation, granule type, and heterogeneities within the granule population under observation".

14 molecules of water per molecule of anhydrous glucose, i.e. a minimum of 75% water, are necessary for full starch gelatinisation (Donovan, 1979). Starch gelatinisation is usually caused by heat, but can be caused by physical damage and some chaotropic agents, mainly dimethylsulphoxide (DMSO), urea, calcium chloride, strong base and acid.

The various events taking place during gelatinisation can be followed by various methods, including birefringence, X-ray diffraction, differential scanning calorimetry (DSC), ¹³C NMR. Swelling can be monitored by various methods, particularly rheology.

Differential scanning calorimetry (DSC) is a destructive method which records an endothermic event on heating of granules, generally thought to measure the temperature and the endothermic energy (ΔH) required for the melting of the native crystallites. Starch gelatinisation temperature is independent of water content above 75% water (described as excess water), but increases when water is limited (Donovan, 1979).

The rate and extent of starch granule swelling upon heating dictate the type of viscosity development of aqueous starch suspensions on heating. Swelling behaviour is therefore of utmost technological importance. Viscosity increase on heating can be conveniently measured by a Brabender amylograph (Brabender is a Trade Mark) (Kennedy and Cabalda, 1991) or using a Rapid Visco analyser (Rapid Visco is a Trade Mark from Newport Scientific, Australia). Figure 1 is a typical viscoamylograph profile for wheat starch, produced in this way, showing changes in starch during and after cooking. As starch granules swell on uptake of water, in a process known as pasting, their phase volume increases, causing an increase in viscosity. The onset of pasting is indicated at A in Figure 1. Peak viscosity, indicated at B in Figure 1, is achieved when maximum phase volume is reached. Shear will then disrupt/cause fragmentation of the swollen granules, causing the viscosity to decrease. Complete dispersion is indicated at C in Figure 1. This has been confirmed by an oscillatory rheology study of starch pastes at various stages of the viscosity profile (Svegmark and Hermansson, 1990). The viscosity onset temperature and peak viscosity are indicative of the initiation and extent of swelling, respectively. On cooling, leached amylose forms a network in a process involving reassociation of molecules, or retrogradation, causing an increase in viscosity as indicated at D in Figure 1. Retrogradation (or set-back) viscosity is therefore indicative of the amount of amylose leached out of the granules.

The properties of wheat starch are useful in a large number of applications and also non-food (paper, textiles, adhesives etc.) applications. However, for many applications, properties are not optimum and various chemical and physical modifications well known in the art are undertaken in order to improve useful properties. Two types of property manipulation which would be of use are: the controlled alteration of gelatinisation and pasting temperatures; and starches which suffer less granular fragmentation during pasting than conventional starches.

Currently the only ways of manipulating the gelatinisation and pasting temperatures of starch are by the inclusion of additives such as sugars, polyhydroxy compounds or salts or by extensive physical or chemical pre-treatments. The reduction of granule fragmentation during pasting can be achieved either by extensive physical pre-treatments

or by chemical cross-linking. Such processes are inconvenient and inefficient. It is therefore desirable to obtain plants which produce starch which intrinsically possesses such advantageous properties.

Starch consists of two main glucose polysaccharides: amylose and amylopectin. Amylose is a generally linear polymer comprising α -1,4 linked glucose units, while amylopectin is a highly branched polymer consisting of an α -1,4 linked glucan backbone with α -1,6 linked glucan branches. In wheat endosperm amylopectin constitutes approximately 70% of the total starch content, with the balance being amylose. Amylopectin is synthesised through the concerted action of several enzymes, including soluble starch synthase(s) (SSS), starch branching enzyme(s) (SBE), starch de-branching enzyme(s) (DBE). The physical properties of starch are strongly affected by the relative abundance of amylose and amylopectin, therefore SSSs, SBEs and DBEs play a key role in determining both starch quantity and quality. As such, one approach to manipulating starch structure would be to modify the expression of the enzymes involved in starch biosynthesis in the endosperm using a transgenic approach.

SBE catalyses the formation of the α -1,6 linkages, creating branch points in the growing starch molecule, via hydrolysis of an α -1,4 linkage followed by reattachment of the released α -1,4-glucan chain to the same or another glucosyl chain. This reaction also provides a new non-reducing end for further elongation of the original α -1,4-glucan chain.

Multiple isoforms of starch branching enzyme have been described; biochemically, from a number of species including maize (Boyer and Preiss, 1978), rice (Nakamura *et al.*, 1992), pea (Smith, 1988), potato (Khoshnoodi *et al.*, 1993) and wheat (Morell *et al.*, 1997). More recently, genomic and cDNA sequences for SBE have been characterised from several species including maize (Baba *et al.*, 1991; Fisher *et al.*, 1993; Gao *et al.*, 1997) pea (Burton *et al.*, 1995), potato (Kossmann *et al.*, 1991), rice (Nakamura and Yamanouchi, 1992; Mizuno *et al.*, 1993), *Arabidopsis* (Fisher *et al.*, 1996), cassava (Salehuzzaman *et al.*, 1992), and wheat (Rapellin *et al.*, 1997, Nair *et al.*, 1997, Rahman *et al.*, 1997). Sequence alignment of these SBEs revealed a high degree of sequence conservation at the amino acid level and that the SBEs may be grouped into two distinct

families, generally known as SBEI and SBEII. Further, analysis indicates that within a species there is generally of the order of 50% homology between the two families, SBEI and SBEII, while there is often greater homology within the two families between species.

Maize is unusual in that the maize SBEII family is thought to comprise two different members, known as SBEIIa and SBEIIb. There has been controversy over whether the SBEIIa and IIb enzymes are in fact a) encoded by genes at two different loci, and b) whether the genes represent different alleles at a single locus. Fisher et al (1996) and Gao et al (1997) have provided evidence that SBEIIa and SBEIIb are encoded by independent genes. However, there is no conclusive evidence that both isoforms exist together in any one maize genotype. The DNA clones for the two published gene sequences were purified from different genotypes of maize and it is thus possible that they represent different alleles of a single locus. In summary, in maize, three distinct SBE genes have been characterised to date (Baba *et al.*, 1991; Fisher *et al.*, 1993; Gao *et al.*, 1997). SBEI is distinct from SBEIIa and SBEIIb in amino acid composition, substrate specificity, kinetic properties, and immunological reactivities, whereas SBEIIa and SBEIIb are similar in these respects (Guan and Preiss, 1993; Preiss 1991; Takeda *et al.*, 1993). At the amino acid level the sequence exhibits approximately 50% homology with the SBEIIa and SBEIIb sequences, whereas SBEIIa and SBEIIb exhibit approximately 80% homology to each other.

Prior to the present invention, maize was unique in having SBEIIa- and SBEIIb-type enzymes. Although *Arabidopsis* has two SBEII family members, the sub-division in *Arabidopsis* does not appear to conform to that seen in maize: the *Arabidopsis* sub-family members do not obviously fall into the IIa and IIb categories as do the maize sequences. Both of the *Arabidopsis* SBEII genes have similar levels of homology to both the maize SBEII genes, SBEIIa and SBEIIb, but the similarities are not sufficient to be able to place the *Arabidopsis* genes into the same SBEIIa and SBEIIb categories as for maize. Indeed, the data, if anything, suggests that the *Arabidopsis* SBEII genes do not fall into the maize IIa and IIb categories. For barley, two forms of SBEII had been partly characterised. Although these have been called SBEIIa and SBEIIb, only a very limited amount of sequence information had been published (Sun *et al*, 1995) and it was not possible to infer

or conclude that these forms correspond to the IIa and IIb categories of maize. In fact, based on the available barley sequence information both of the barley SBEII sequences (SBEIIa and SBEIIb) would appear to show greater homology to maize SBEIIa than to maize SBEIIb.

For all other plant species for which SBEII sequences have been identified and published, including potato, pea, rice, cassava, wheat and barley, no sub-division of the SBEII family comparable to the SBEIIa and SBEIIb division of maize has been made.

Studies of purified SBEI and SBEII demonstrate that these isoforms differ in their specificity for a substrate with respect to both chain length and degree of branching. In maize, SBEI and SBEII show distinct branching activities *in vitro*, with SBEI showing a higher rate of branching of an amylose substrate when compared to SBEII whereas both SBEIIa and IIb show higher rates of branching than SBEI when acting upon an amylopectin substrate (Guan and Preiss, 1993). Furthermore, maize SBEI preferentially transfers longer glucan chains (average chain length = 24) than SBEII (average chain length = 21(IIa) and 22(IIb)) (Takeda *et al.*, 1993). A similar observation has been reported for SBEI and SBEII isoforms from wheat and pea (Morell *et al.*, 1997; Smith, 1988). Mutational studies in maize, rice and pea demonstrate that high amylose mutants in each case are deficient in the branching enzyme activity analogous to maize SBEII (Martin and Smith, 1995; Morell *et al.*, 1995). However, the linkage between the biochemical observations and the genetic evidence suggesting the differences in the roles remains unclear.

The present invention is based on the unexpected discovery of a novel class of SBEII genes in wheat, referred to herein as SBEII-1. The novel SBEII-1 gene sequence has strong homology with the maize SBEIIb gene. The wheat SBEII-1 genes are thought to be functionally equivalent to the maize SBEIIb gene, and on this basis it is believed that manipulation of the wheat SBEII-1 gene is likely to influence starch properties including starch gelatinisation temperature, in a manner analogous to manipulation of the maize SBEIIb gene as described in WO 97/22703.

In summary, although two different SBEII gene sequences are known from maize, Arabidopsis and barley, as discussed above, prior to the present invention there was no reason to expect that wheat would show a similar sub-division of SBEII genes as is seen for maize. The two Arabidopsis SBEII genes show a different sub-division, and prior to the present invention there was insufficient evidence to determine whether the two barley SBEII sequences belonged to the maize-type sub-division. That is, prior to the present invention there was no reason to expect that wheat would have two similar SBEII members comparable to those of maize. Subsequent to the present invention Sun et al (1998) have presented data which indicates that the barley sequences do indeed sub-divide in a similar manner to the maize SBEIIa and IIb sequences and the wheat SBEII-2 and SBEII-1 sequences discussed in this document.

The present inventors have used the high degree of sequence conservation between several SBE gene sequences to design oligonucleotide primers to motifs which are specific to either SBEI or SBEII families and have used these primers to amplify cDNA sequences from developing endosperm of wheat.

When this work was started, a single partial length wheat SBE cDNA clone had been reported (Mousley, 1994). Multiple sequence alignment of this wheat SBE sequence with other published SBE sequences from a number of plant species revealed a number of motifs which were highly conserved. Oligonucleotide primers designed to be complementary to these motifs were used to clone 3' partial length cDNA clones of wheat SBEII. Alignment of the cDNA clone sequences indicated that the clones could be divided into two classes, which the inventors have designated SBEII-1 and SBEII-2, which showed greater than 90% similarity to members within a class but only 60% similarity between classes. Significantly, comparison between representative sequences from each class with previously identified wheat SBEII clones, pWBE6 (Mousley, 1994) and SBEII (Nair *et al.*, 1997), showed that each appear to be homologues of the SBEII-2 class. The cloning of a wheat SBEII-1 cDNA is novel.

Summary of the Invention

In one aspect the invention provides a nucleotide sequence encoding substantially the amino acid sequence shown in Figure 10 (SEQ ID No: 2) or a functional equivalent of said nucleotide sequence.

The term functional equivalent is used in this context to encompass those sequences which differ in their nucleotide composition to that shown in Figure 10 (SEQ ID No: 1) but which, by virtue of the degeneracy of the genetic code, encode polypeptides having identical or substantially identical amino acid sequences. It is intended that the term should generally apply to sequences which are sufficiently homologous to the sequence of the invention that they can hybridise to the complement thereof under stringent hybridisation conditions (eg as described by Sambrook et al 1989, ie washing with 0.1xSSC, 0.5% SDS at 68°C); such equivalents will preferably possess at least 86%, more preferably at least 90%, and most preferably at least 95%, sequence homology (ie sequence similarity) with the sequence of the invention. Sequence homology is suitably determined using the 'MEGALIGN' program of the software package DNASTar (MEGALIGN and DNASTar are Trade Marks). It will be apparent to those skilled in the art that the nucleotide sequence of the invention may also find useful application when present as an "antisense" sequence. Accordingly, functionally equivalent sequences will also include those sequences which can hybridise, under stringent hybridisation conditions, to the sequence of the invention (rather than the complement thereof). Such "antisense" equivalents will preferably possess at least 86%, more preferably at least 90%, and most preferably 95% sequence homology with the complement of the sequence of the invention.

In another aspect, the invention provides a nucleotide sequence comprising substantially the sequence of B2 shown in Figure 3 (SEQ ID No: 3), or a functional equivalent thereof.

In a further aspect, the invention provides a nucleotide sequence comprising substantially the sequence of B4 shown in Figure 3 (SEQ ID No: 4), or a functional equivalent thereof.

Another aspect of the invention provides a nucleotide sequence comprising substantially

the sequence of B10 shown in Figure 3 (SEQ ID No: 5), or a functional equivalent thereof.

Yet a further aspect of the invention provides a nucleotide sequence comprising substantially the sequence of B1 shown in Figure 3 (SEQ ID No: 6), or a functional equivalent thereof.

In another aspect the invention provides a nucleotide sequence encoding substantially the amino acid sequence of B6 shown in Figure 4 (SEQ ID No: 7), or a functional equivalent thereof.

The term functional equivalent in this context has the same general meaning as discussed above, although equivalents for B2, B4, B10 and B6 will preferably possess at least 90%, more preferably at least 95%, sequence homology with the relevant sequence of the invention, while equivalents for B1 will preferably possess at least 97% sequence homology with the sequence of the invention.

The sequences of the invention are part of novel wheat SBEII genes, with B1 being a novel subclass of the known class of SBEII genes, referred to herein as SBEII-2, with the novel subclass being called SBEII-2B. The remaining sequences are all of a completely new class of wheat SBEII genes, referred to herein as SBEII-1. The sequences have been found to fall into 3 sub-classes, to be discussed below.

The novel wheat SBEII-1 genes that are the subject of this invention have strong sequence homology with the maize SBEIIb gene. The wheat SBEII-1 genes are thought to have similar functional properties to the maize SBEIIb gene. On this basis it is expected that by genetic manipulation of the wheat SBEII-1 gene it will be possible to influence properties of starch produced by a plant, including the gelatinisation temperature and rheological properties of starch, in a manner analogous to manipulation of the maize SBEIIb gene described in WO 97/22703. The content of WO 97/22703 is incorporated herein by reference.

The present invention also includes within its scope a portion of any of the above sequences, comprising at least 500 base pairs and having at least 90% sequence homology to the corresponding portion of the sequence from which it is derived.

Although the coding sequences of the novel wheat SBEII-1 genes have strong sequence homology with the maize SBEIIb gene, there is much greater divergence in the 3' untranslated parts of the sequences, with a maximum of 31.8% homology between the 3' untranslated sequences of wheat SBEII-1 and maize SBEIIb as is apparent from Figure 8.

In another aspect the invention thus provides a nucleotide sequence comprising substantially the sequence shown in Figure 5 (SEQ ID No: 8), Figure 6 (SEQ ID No: 9) or Figure 7 (SEQ ID No: 10), or a functional equivalent thereof.

The term functional equivalent in this context has the same general meaning as discussed above, but with equivalents preferably at least 32%, more preferably at least 40%, 50%, 60%, 70%, 80% or 90% sequence homology with the sequence of the relevant Figure.

It is thought such 3' untranslated sequences may be useful, both in sense and antisense function, in manipulation of starch properties by affecting SBE expression in plants, as will be discussed below.

The sequence may include further nucleotides at the 5' or 3' end. For example, for ease of expression, the sequence desirably also comprises an in-frame ATG start code, and may also encode a leader sequence.

The invention also covers a nucleic acid construct comprising a nucleotide sequence or portion thereof in accordance with the invention conveniently operably linked, in sense or antisense orientation, to a promoter sequence.

Also included within the scope of the invention is amino acid sequence encoded by any of the nucleotide sequences of the invention.

The invention also provides vectors, particularly expression vectors, comprising the nucleotide sequence of the invention. The vector will typically comprise a promoter and one or more regulatory signals of the type well known to those skilled in the art. The invention also includes provision of cells transformed (which term encompasses transduction and transfection) with a vector comprising the nucleotide sequence of the invention.

Nucleotide sequences in accordance with the invention may be introduced into plants, particularly but not exclusively wheat plants, and it is expected that this can be used to affect expression of SBE in the plant and hence affect the properties of starch produced by the plant. In particular, use of sequences in antisense orientation is expected to reduce or suppress enzyme expression. Additionally, it has recently been demonstrated in other experimental systems that "sense suppression" can also occur (i.e. expression of an introduced sequence operably linked in the sense orientation can interfere, by some unknown mechanism, with the expression of the native gene), as described by Matzke & Matzke 1995. Any one of the methods mentioned by Matzke & Matzke could, in theory, be used to affect the expression in a host of a homologous SBE gene.

It is believed that antisense methods are mainly operable by the production of antisense mRNA which hybridises to the sense mRNA, preventing its translation into functional polypeptide, possibly by causing the hybrid RNA to be degraded (e.g. Sheehy *et al.*, 1988; Van der Krol *et al.*). Sense suppression also requires homology between the introduced sequence and the target gene, but the exact mechanism is unclear. It is apparent however that, in relation to both antisense and sense suppression, neither a full length nucleotide sequence, nor a "native" sequence is essential. Preferably the "effective portion" used in the method will comprise at least one third of the full length sequence, but by simply trial and error other fragments (smaller or larger) may be found which are functional in altering the characteristics of the plant.

Thus, in a further aspect the invention provides a method of altering the characteristics of a plant, comprising introducing into the plant an effective portion of the sequence of the invention operably linked to a suitable promoter active in the plant so as to affect

expression of a gene present in the plant. Conveniently the sequence will be linked in the antisense orientation to the promoter. Preferably the plant is a wheat plant. Conveniently, the characteristic altered relates to the starch content and/or starch composition of the plant (i.e. amount and/or type of starch present in the plant). Preferably the method of altering the characteristics of the plant will also comprise the introduction of one or more further sequences, in addition to an effective portion of the sequence of the invention. The introduced sequence of the invention and the one or more further sequences (which may be sense or antisense sequences) may be operably linked to a single promoter (which would ensure both sequences were transcribed at essentially the same time), or may be operably linked to separate promoters (which may be necessary for optimal expression). Where separate promoters are employed they may be identical to each other or different. Suitable promoters are well known to those skilled in the art and include both constitutive and inducible types. Examples include the CaMV 35S promoter (e.g. single or tandem repeat) and the ubiquitin promoter. Advantageously the promoter will be tissue-specific. Desirably the promoter will cause expression of the operably linked sequence at substantial levels only in the tissue of the plant where starch synthesis and/or starch storage mainly occurs.

The sequence of the invention, and the one or more further sequences if desired, can be introduced into the plant by any one of a number of well-known techniques (e.g. *Agrobacterium*-mediated transformation, or by "biolistic" methods). The sequences are likely to be most effective in affecting SBE activity in wheat plants, but theoretically could be introduced into any plant. Desirable examples include pea, tomato, maize, rice, barley, sweet potato and cassava plants. Preferably the plant will comprise a natural gene encoding an SBE molecule which exhibits reasonable homology with the introduced nucleic acid sequence of the invention.

In another aspect, the invention provides a plant cell, or a plant or the progeny thereof, which has been altered by the method defined above. The progeny of the altered plant may be obtained, for example, by vegetative propagation, or by crossing the altered plant and reserving the seed so obtained. The invention also covers parts of the altered plant, such as storage organs. Conveniently, for example, the invention covers grain comprising

altered starch, said grain being obtained from an altered plant or the progeny thereof. Grain obtained from altered plants (or the progeny thereof) will be particularly useful materials in certain industrial applications and for the preparation and/or processing of foodstuffs and may be used, for example, in bakery products.

In particular relation to wheat plants, the invention provides a wheat plant or part thereof which, in its wild type possesses an effective SBEII-1 gene, but which plant has been altered such that there is either reduced, increased or no effective expression of an SBEII-1 polypeptide within the cells of at least part of the plant. The plant may have been altered by the method defined above, or may have been selected by conventional breeding to be deleted for the SBEII-1 gene, the presence or absence of which can be readily determined by screening samples of the plants with a nucleic acid probe or antibody specific for the wheat gene or gene product respectively.

The invention also provides starch extracted from a plant altered by the method defined above, or from the progeny of such a plant, the starch having altered properties compared to starch extracted from equivalent, but unaltered, plants. The invention further provides a method of making altered starch, comprising altering a plant by the method defined above and extracting therefrom starch having altered properties compared to starch extracted from equivalent, but unaltered, plants. It is believed that use of nucleotide sequences in accordance with the invention will enable the production of starches, particularly wheat starches, having a wide variety of novel properties. For example, it may be anticipated that plants altered to give a reduction in SBEII activity will give rise to a starch with a relatively higher proportion of amylose and a lower proportion of amylopectin compared with that from unaltered plants.

In particular the invention provides the following: a plant (especially a wheat plant) altered by the method defined above, containing starch which, when extracted from the plant, has an elevated gelatinisation onset and/or peak temperature as measured by DSC, compared to starch extracted from a similar, but unaltered, plant; a plant (especially a wheat plant) altered by the method defined above, containing starch which, when extracted from the plant, has a elevated gelatinisation onset temperature (conveniently elevated by at least

3°C, possibly by at least 7°C, by at least 12°C or possibly even by 15 to 25°C) as measured by DSC compared to starch extracted from a similar, but unaltered plant; a plant (especially a wheat plant) altered by the method defined above, particularly to reduce expression of SBEII-1 polypeptide, containing starch which, when extracted from a plant, has a higher amylose:amylopectin ratio compared to starch extracted from a similar, but unaltered plant.

The present invention particularly covers starch extracted from a plant altered by the method of the invention, particularly starch having an increased gelatinisation temperature. Such starch is useful, eg in bakery products, having particular benefits in certain situations, and the invention also covers products, particularly bakery products, made from such starch. The invention also covers starch extracted from a plant altered by the method of the invention and having an increased amylose:amylopectin ratio.

The invention will be further described, by way of illustration, in the following Examples and with reference to the accompanying drawings, in which:

Figure 1 is a graph of viscosity versus time, showing a viscoamylgraph profile for wheat starch during and after cooking;

Figure 2 shows alignment amino acid sequence data of C terminal portions of various known starch branching enzymes (SEQ ID Nos: 12 to 25), obtained from the European Molecular Biology Laboratory (EMBL) database, and for a novel wheat SBEII-1 sequence of the invention (OsbeII-1ALL) (SEQ ID No: 11) from clone 5A1, with consensus residues highlighted;

Figure 2a is a residue weight table showing the percent similarity and percent divergence of the sequences shown in Figure 2;

Figure 3 shows aligned DNA sequence data for various recombinant clones (B2, B4, B10, A2, B1, B11) (SEQ ID Nos: 3, 4, 5, 26, 6, 27 respectively) containing wheat starch branching enzyme genes, representing two SBE classes, SBEII-1 and SBEII-2, each of

which includes three subclasses A, B and C, with residues differing from the consensus (majority) (SEQ ID No: 53) highlighted;

Figure 3a is a residue weight table showing the percent similarity and percent divergence of the sequences shown in Figure 3;

Figure 4 is an alignment of predicted amino acid sequences for clones B6 (wheat SBEII-1) (SEQ ID No: 7) and B11 (wheat SBEII-2) (SEQ ID No: 28) against the corresponding regions of the maize SBEIIa (SEQ ID No: 29) and SBEIIb (SEQ ID No: 30) amino acid sequences, with residues differing from those of maize SBEIIb highlighted;

Figure 4a is a residue weight table showing the percent similarity and percent divergence of the sequences shown in Figure 4;

Figure 5 shows the 3' untranslated DNA sequence of clone B2 (SEQ ID No: 8) (wheat SBEII-1, sub-class A);

Figure 6 shows the 3' untranslated DNA sequence of clone B10 (SEQ ID No: 9) (wheat SBEII-1, sub-class B);

Figure 7 shows the 3' untranslated DNA sequence of clone B4 (SEQ ID No: 10) (wheat SBEII-1, sub-class C);

Figure 8 shows aligned DNA sequence data for the 3' untranslated region of clones B10 (SEQ ID No: 9), B2 (SEQ ID No: 8) and B4 (SEQ ID No: 10) and maize SBEIIb (ZMSBE2b) (SEQ ID No: 31), with residues differing from those of the B10 sequence highlighted;

Figure 8a is a residue weight table showing the percent similarity and percent divergence of the sequences shown in Figure 8;

Figures 9a and 9b show hybridisation of clone B1 (SBEII-2) and clone B2 (SBEII-1),

respectively, to HindIII-digested genomic DNA of Chinese Spring wheat nullisomic-tetrasomic lines;

Figure 10 shows the DNA (SEQ ID No: 1) and predicted amino acid sequence (SEQ ID No: 2) of part of SBEII-1 clone 5A1;

Figure 11 shows aligned amino acid sequence data for the wheat SBEII-1 sequence of the invention, from clone 5A1 (OsbeII-1ALL) (SEQ ID No: 11), wheat SBEI-D2 (SEQ ID No: 32) of Rahman *et al* 1997 (TASBEID2), wheat SBE1 of Rapellin *et al* 1997 (SEQ ID No: 33) (TASBEI) and wheat SBEII-2 of Nair *et al* 1997 (SEQ ID No: 34) (wheat SBEII-2), with residues exactly matching the consensus (majority) (SEQ ID No: 54) highlighted;

Figure 11a is a residue weight table showing the percent similarity and percent divergence of the sequences shown in Figure 11;

Figure 12 illustrates northern blotting of wheat grains harvested at various different intervals after anthesis and probed with SBEII-1 and SBEII-2 fragments;

Figure 13 is a restriction map of plasmid pWxGS+;

Figure 13a shows the sequence (SEQ ID No: 55) of the promoter (HindIII-BamHI fragment) in pWxGS+;

Figure 14 is a restriction map of plasmid pSRWXGUS1;

Figure 15 is a restriction map of plasmid pVTWXGUS2;

Figure 16 is a restriction map of plasmid pPBI-97-2;

Figure 17 is a restriction map of plasmid pSR97-26A-;

Figure 18 is a restriction map of plasmid pSR97-29A-;

Figure 19 is a restriction map of plasmid pSR97-50A-;

Figure 20 is a restriction map of plasmid pSR97-53A-;

Figure 21 is a restriction map of plasmid p97-2C;

Figure 22 is a restriction map of plasmid p97-2CWT1;

Figure 23 is a restriction map of plasmid pSC98-1;

Figure 24 is a restriction map of plasmid pSC98-2;

Figure 25 is a restriction map of plasmid pUNI;

Figure 26 shows the DNA sequence of the NptII SacI fragment of pUNI (SEQ ID No: 35); and

Figure 27 is a restriction map of plasmid pUSN99-1;

Figure 28 is a restriction map of plasmid pUSN99-2;

Figure 29 is a partial restriction map of the predicted sequence (SEQ ID No: 52) of a cloned fragment of p97-U3;

Figure 30 is a restriction map of plasmid pPBI96-36;

Figure 31 is a restriction map of plasmid p97-dUG1;

Figure 32 is a restriction map of plasmid p97-2BdUN1;

Figure 33 is a schematic illustration of a particle bombardment chamber (not to scale);

Figure 34 shows histochemical localisation of Ubi-GUS expression in seed (panel A), stem (panel B), floral (panel C) and leaf tissues (panel D) of wheat transformed with plasmid pAHC25;

Figure 35 is a Southern blot of 26 progeny plants of transformant BW119 which had been transformed with pAHC25.

Figure 36 shows histochemical localisation of waxy-GUS expression in endosperm tissue of two independent transgenic wheat lines (in panels A and B) transformed with the plasmid pWxGS+; and

Figure 37 is a Southern blot of genomic DNA of putative primary transformants digested with SacI and probed with the 1kb SacI SBEII-1 probe.

Examples

Amplification and characterisation of two classes of SBEII cDNA clones

A PCR based cloning strategy was devised for isolating starch branching enzymes from wheat using conserved domains within the known cloned gene sequences. Starch branching enzymes have been cloned from a number of plant species and Figure 2 shows amino acid sequence data, obtained from the European Molecular Biology Laboratory (EMBL) nucleotide database for various known starch branching enzymes as follows:-

Wheat SBEII-2 for *Triticum aestivum* (SEQ ID No: 12)

ZM SBE2a (maize) for *Zea mays* (SEQ ID No: 13)

ZM SBE2b (maize) for *Zea mays* (SEQ ID No: 14)

Barley SBEIIa (SEQ ID No: 15)

Barley SBEIIb (SEQ ID No: 16)

RICBCE3 (rice SBEII type enzyme) for *Oryza sativa* (SEQ ID No: 17)

RICESBE-1/97 (as above, including transit peptide sequence) (SEQ ID No: 18)
PSSBEIGEN (pea SBEI, which is in fact an SBEII- type sequence) for *Pisum sativum* (SEQ ID No: 19)
STSBE (potato SBEI type) for *Solanum tuberosum* (SEQ ID No: 20)
TASBEI (wheat SBEI-2) for *Triticum aestivum* (SEQ ID No: 21)
TASBEI D2 (SEQ ID No: 22)
ZMSBEI (maize SBEI) for *Zea mays* (SEQ ID No: 23)
RICBEI (rice SBEI) for *Oryza sativa* (SEQ ID No: 24)
PSSBEIIGN (pea SBEII, which is in fact an SBEI-type sequence) for *Pisum sativum* (SEQ ID No: 25)

Figure 2 also shows sequence information for a novel wheat SBEII-1 sequence of the invention, identified as OsbeII-1ALL (SEQ ID No: 11).

The alignment report of Figure 2, and also Figures 3, 4, 8 and 11, was prepared using Clustal method, with PAM 250 residue weight table for amino acid sequences and weighted residue weight table for DNA sequences. Sequence pair distances expressed as % similarity shown in Figures 2A and 3A, 4A, 8A and 11A are determined using a 'MEGALIGN' program of DNASTar software, and correspond to sequence homology percentages as specified above.

Alignment of the sequences shown in Figure 2 reveals several domains which are highly conserved. One such domain, MDKDMYD (SEQ ID No: 36), was almost completely conserved and it was assumed that this domain would also be present in wheat starch branching enzyme genes. This motif was chosen as a target for an oligonucleotide sense primer (SBEA). 3'RACE PCR was carried out on endosperm first strand cDNA using the primers Ro and SBE A.

Two populations of PCR products of approximately 1kb and 1.2Kb were cloned into the plasmid vector pT7Blue (Novagen). Plasmid DNA from 36 putative recombinant clones was purified and the insert size estimated by restriction analysis. Fifteen clones harbouring inserts of between approximately 1Kb and 1.2Kb were selected for sequencing.

Alignment of the sequence data obtained, using the MEGALIGN program of DNASTar, indicated that the 15 selected clones could be divided on the basis of degrees of homology into two different classes, which we have designated SBEII-1 and SBEII-2. Furthermore, both the SBEII-1 and SBEII-2 classes may each be further subdivided into three sub-classes, based on sequence differences (Table 1). It is thought the sub-division into three sub-classes probably arises because wheat comprises three homoeologous genomes.

Table 1

Class	Sub-Class	Clone Number
SBEII-1	A	B2, B5, B6, B7, B12
SBEII-1	B	B10
SBEII-1	C	A1, A13, B4
SBEII-2	A	B11
SBEII-2	B	B1, B9
SBEII-2	C	A2, C5

Comparison between sequences within either of the SBEII-1 or SBEII-2 classes showed between 90 and 96.8% similarity. In contrast, sequence similarity between representatives of SBEII-1 and SBEII-2 classes only display between 58.8 and 60.0% homology in the region of comparison (Figures 3 and 3a).

Furthermore, we have compared representative sequences from each SBEII-1 and SBEII-2 class with the previously reported wheat SBEII clones, pWBE6 (Mousley, 1994) and the very recently published SBEII (Nair *et al.*, 1997). The results showed that each of the previously isolated SBEII clones are highly homologous (>90%) to our SBEII-2 class (data not shown). Significantly, neither of the previously reported wheat sequences showed high homology to our SBEII-1 sequence. The isolation and characterisation of three forms of SBEII-1 (SBEII-1, sub-classes A, B & C) is novel. The SBEII-2 sub-class B is also novel, sub-classes A and C corresponding to the sequences previously disclosed by Mousley (1994) and Nair *et al* (1997) respectively.

Alignment of the predicted amino acid sequences from representative clones, B6 and B11 of the wheat SBEII-1 and SBEII-2 sequences (respectively) against the corresponding regions of the maize SBEIIa and SBEIIb amino acid sequences (Figure 4 and 4a) indicate that the wheat SBEII-1 sequence (clone B6) is more similar to the maize SBEIIb sequence (88.7% similarity) than to the wheat SBEII-2 sequence and the maize SBEIIa sequence (82.2% & 82.6% similarity respectively) and similarly that the wheat SBEII-2 sequence is more similar to the maize SBEIIa sequence (86.9% similarity) than to the wheat SBEII-1 and maize SBEIIb sequences (82.2% and 81.7% similarity respectively). We thus hypothesise that the wheat SBEII-1 is phylogenetically more related to the maize SBEIIb and that the wheat SBEII-2 is phylogenetically related to the maize SBEIIa sequences and that the corresponding wheat and maize sequences are likely to exhibit similar functional properties.

While the coding sequences of clones B2, B10 and B4 have strong sequence homology to the maize SBEIIb gene, there is much greater divergence in the 3' untranslated parts of the sequences. Figure 5, 6 and 7 show the 3' untranslated sequences of clones B2, B10 and B4, respectively, and Figure 8 compares these sequences with the corresponding sequence of maize SBEIIb.

Considering matters in more detail, experimental details were as follows.

Plant material

Triticum aestivum cultivar Rialto was grown in a glass house under supplementary lighting and temperature control to maintain a 16 hour day-length at 18 \pm 1°C.

Recombinant DNA manipulations and sequencing

Standard procedures were performed essentially according to Sambrook *et al.*, (1989). DNA sequencing was performed on an ABI automated sequencer and sequences analysed using DNASTAR software for Macintosh.

RNA isolation for cDNA cloning

RNA was extracted from *Triticum aestivum* cultivar Rialto endosperm, using a Purescript RNA isolation kit (Flowgen) essentially according to the manufacturers recommendations. Briefly, endosperm tissue was frozen in liquid nitrogen and ground, for 2 min, to a fine powder using a dismembrator (Braun Biotech International). The ground tissue was stored in liquid nitrogen prior to extraction. Approx. 100mg of ground tissue was transferred to a 1.5ml microcentrifuge tube and 1.2ml of 'Lysis buffer' was added to the tissue before mixing by inversion and placing on ice for 10 minutes. Protein and DNA were precipitated from the cell lysate by adding 0.4ml of 'Protein-DNA Precipitation Solution' and mixing by inversion before centrifuging at 13,000 x g at 4°C for 20 minutes. The supernatant was divided between two fresh 1.5ml tubes each containing 600µl of *iso*-propanol. The RNA precipitate was pelleted by centrifugation at 13,000 x g at 4°C for 10 minutes, the supernatant was discarded and the pellets washed with 70% ethanol by inverting the tube several times. The ethanol was discarded and the pellet air dried for 15-20 minutes before the RNA was resuspended in 7.5ml of 'RNA Hydration Solution'.

Preparation of wheat endosperm cDNA pool

Wheat endosperm cDNA pool was prepared from total RNA, extracted as described above, using Superscript™ reverse transcriptase (Life Technologies) essentially according to manufacturers instructions. Briefly, five microgrammes of RNA, 10pMol RoRidT17 [AAGGATCCGTCGACATCGATAATACGACTCACTATAGGGA(T17)] (SEQ ID No: 37) and sterile distilled water to a reaction volume of 12µl, in a 500µl microcentrifuge tube, was heated to 70°C for 10 minutes before being quick chilled on ice. The contents of the tube were collected by brief centrifugation before adding 4µl 5x First Strand Buffer, 2µl 0.1M DTT and 1µl 10mM dNTPs and, after mixing, incubating at 42°C for 2 min. 1µl of Superscript™ was added and, after mixing, incubation continued for 1 hour. The reaction was inactivated by heating to 70°C for 15 min. 150µl of T₁₀E₁ was added to the reaction mix and the resulting cDNA pool was used as a template for amplification in PCR.

PCR amplification of SBEII sequences from endosperm cDNA pool

SBEII sequences were amplified from the endosperm cDNA pool using primers Ro [AAGGATCCGTCGACATC] (SEQ ID No: 38), which is complementary to the Ro region of the RoRidT17 primer used to synthesise the cDNA pool, and the SBEII specific primer, SBEA [ATGGACAAGGATATGTATGA] (SEQ ID No: 39). SBEA was designed to be homologous to the MDKDMYD (SEQ ID No: 36) motif which is situated approx. 1kb from the 3' end of the mature peptide coding sequence. PCR was carried out in a 50 μ l reaction, comprising 5 μ l of the cDNA pool, 25pmol Ro, 50pmol SBEA, 5 μ l 5x Taq buffer, 4 μ l 25mM Mg²⁺, 0.5 μ l 20mM dNTPs, and 1.25u Taq polymerase. All of the reaction components were mixed, except for the Taq polymerase, before being pre-heated to 94°C for 7 min and then cooled to 75°C for 5 min. Whilst the reaction mixtures were held at 75°C the Taq polymerase was added and, after mixing well, the reactions were thermocycled at (94°C-30sec, 50°C-30sec, 72°C-1min) x 30 cycles, followed by a final 10 min extension step at 72°C.

PCR products were purified by phenol/chloroform and chloroform extraction before ligation with pT7 Blue (Novagen) according to manufacturers recommendations. Putative SBE clones were initially characterised by standard plasmid DNA purification methods and restriction digestion. Representative clones harbouring a range of different sized inserts were selected for sequencing.

Chromosomal location of SBE genes in wheat

The Chinese Spring wheat nullisomic-tetrasomic lines as described in Sears (1966) were used for assignment of the SBE sequences chromosome locations. Ditelosomic lines (Sears, 1966) were used to determine the chromosome arm location. The Betzes barley ditelosomic addition lines in wheat are described in Islam (1983).

The chromosomal location of the two families of SBEII sequences (SBEII-1, SBEII-2) was determined by probing wheat nulli-tetra and ditelosomic stock lines with gel-purified inserts of the various clones. Figure 9a shows the hybridisation obtained with an SBEII-2

(clone B1) probe on HindIII digested DNA. The euploid Chinese Spring gives 3 bands, one of which is missing in turn in the lines nullisomic for chromosomes 2A, 2B and 2D. The same blot was re-probed with a SBEII-1 specific probe (clone B2). This yields an entirely different hybridisation profile (Figure 9b), demonstrating the specificity of the probe used. Again bands are missing in each of the lines nullisomic for 2A, 2B and 2D. the same banding pattern was observed using the SBEII-1 clones B2 and B4. Thus the SBEII sub-family 1 and 2 gene sequences lie on the wheat group 2 set of homeologous chromosomes.

Ditelosomic addition lines were used to identify the arm location of these genes (data not shown). This revealed that the SBEII-1 and SBEII-2 sequences are both located on the long arms of the homeologous group 2 chromosomes of wheat.

Barley addition lines were used to determine whether homologous sequences are present in barley. These showed that sequences homologous to the wheat SBEII-1 and SBEII-2 sequences are located on the long arms of barley chromosome 2H.

RNA Isolation and Northern Blotting

Wheat grains were harvested at appropriate intervals and frozen in liquid Nitrogen before grinding to a fine powder using either a Braun Mikrodismembrator™ or a pestle and mortar. Total RNA was isolated using the RNAqueous™ (Ambion Inc) Kit according to the manufacturers instructions, or with the following method. Frozen powdered grain was mixed with a 10X volume of 0.2M Tris-HCl pH9, 0.4M NaCl, 25mM EDTA, 1% SDS, 1% PVPP, 0.25% Antifoam A, and 0.1M DTT. This mixture was extracted twice with an equal volume of phenol/chloroform/isoamyl alcohol (25:24:1), the nucleic acids precipitated from the aqueous phase by the addition of 0.8 volumes of isopropanol, and the resulting pellet dissolved in H₂O. The RNA was then selectively precipitated by the addition of 1 volume of 4M LiCl, incubated at 4°C overnight, and the resulting pellet dissolved in sterile distilled H₂O. 15 µg of total RNA was electrophoresed on a 1% agarose, 2.21M Formaldehyde, 40mM MOPS pH7.0, 10mM sodium acetate, 1mM EDTA gel, in a 40mM MOPS pH7, 10mM sodium acetate, 1mM EDTA running buffer at 1

V/cm overnight. Gels were placed in a 50ng/ml solution of Ethidium Bromide in water for 30 minutes, de-stained in water for 2 hours, and visualised and photographed under UV light. The gels were then washed briefly in sterile distilled H₂O, then blotted onto HyBond N⁺™ (Amersham International), according to standard protocols (Sambrook et al, 1989) overnight. Blots were then dismantled and air-dried before UV fixing at 312nm for 2 minutes.

Probe Isolation and Purification

5-10 µg of the plasmids pUN1 and pSR98-29 were digested with SstI (Life Technologies Ltd) according to the manufacturers instructions, to release fragments of approximately 0.8kb (NptII) and 1kb (SBEII-1) respectively. 5-10µg of the plasmid pVT96-54 was digested with BamHI to release a SBEII-2 fragment of approximately 1.2kb. Digests were electrophoresed on 1% low melting point agarose gels. The gene specific fragments were excised and the DNA purified using a Wizard™ Gel Purification Kit (Promega).

Probe Labelling and Hybridization

25ng of the appropriate probe (Maize Waxy promoter, NptII, Wheat SBEII-1 or Wheat SBEII-2 fragments) were radiolabelled using the Rediprime 11™ system (Amersham International) using α³²PdCTP (Amersham International) according to manufacturers instructions. Blots were hybridized overnight at 65°C in 0.6M NaCl, 20mM Pipes, 4mM Na₂EDTA.2H₂O, 0.2% gelatin, 0.2% Ficoll 400, 0.2% PVP-360, 10mM Na₄P₂O₇.10H₂O, 0.8% SDS, 0.5mg/ml denatured salmon sperm DNA. Post hybridization washes were carried out in 30mM NaCl, 2mM NaH₂PO₄.2H₂O, 0.2mM Na₂EDTA.2H₂O, 0.1% SDS at room temperature for 7 minutes, then 65°C for 10 minutes. Filters were exposed to Kodak BioMax MR™ (Amersham International) film at -70°C. Blots were stripped by washing in 15mM NaCl, 1mM NaH₂PO₄.2H₂O, 0.1mM EDTA at 90°C for 10 minutes, or until no counts above background remained.

Extension of the SBEII-1 3' sequence towards the 5' end of the mature peptide

We have exploited the sequence divergence between our wheat SBEII-1 and SBEII-2 sequences to design the SBEII-1 specific 3' primer, Sb4. This primer was used in conjunction with an SBEII specific 5' primer to extend the novel SBEII-1 sequence using a PCR-based approach.

To extend the SBEII-1 3' sequence towards the 5' end of the mature peptide, a second conserved domain was identified and an oligonucleotide sense primer, AGSBEI, designed. PCR amplification from the endosperm first strand cDNA pool was carried out using the AGSBEI-Sb4 primer pair. Separation of the amplification products by electrophoresis through a 1% (w/v) agarose gel (data not shown) showed that the reaction yielded a distinct band of approx. 2.2kb. The approx 2.2kb amplification products were excised from the gel, ligated with PT7Blue and transformed into competent Novablue *E. coli* cells. Following overnight culture, nine putative recombinant clones were selected for further analysis. Screening of each of the selected clones using vector specific primers indicated that clones 5A1, 5A2, 5A5 and 5A9 harboured inserts of the predicted size. Of these clone 5A1 (which falls in sub-class C) was selected for sequencing (Figure 10). The amino acid sequence of Figure 10 corresponds to the OsbeII-1ALL sequence of Figure 2. Although not full length the predicted open reading frame includes nucleotides 44 through to 1823 and encodes a 593 amino acid peptide. Based on similarities with the maize genes, it is estimated that this sequence is missing approximately 230 amino acids out of a predicted total of approximately 830 amino acids. On this basis, the partial sequence represents about 70% of the coding sequence. Multiple sequence alignment of this SBEII-1 sequence with recently published wheat SBEII-2 (Nair *et al.*, 1997), SBEI (Rapellin *et al.*, 1997) and SBEI-D2 (Rahman *et al.*, 1997) sequences showed that the SBEII-1 sequence has similarity indices of 69.6%, 31.2% and 46.7% to SBEII-2, SBEI and SBEI-D2 respectively (Figures 11 and 11a). This demonstrates that the SBEII-1 sequence differs from the published wheat SBE sequences, and confirms the analysis of the 3' sequence alignment (Figure 3). The increase in relative homology when compared to the values obtained following 3' sequence alignment results from the fact that the central domain of SBEs is highly conserved (Burton *et al.*, 1995; Gao *et al.*, 1997). However, it is clear

that this cloned wheat SBEII-1 sequence is significantly different from previously published wheat SBE sequences and represents a novel sequence.

Full experimental details were as follows.

SBEII-1 sequences were extended toward the 5' end of the mature peptide by amplification from the endosperm cDNA pool using the SBEII-1 specific primer Sb4 [TTTTCTTCACAACGCCCTGGG] (SEQ ID No: 40) in conjunction with the primer AGSBEI [TGTTTGGGAGATCTTCCTCCC] (SEQ ID No: 41). AGSBEI was designed to be homologous to the GVWEIFLP (SEQ ID No: 42) motif which is conserved in all known SBE sequences and is situated toward the 5' end of the mature peptide coding sequence. PCR was carried out in a 50 μ l reaction, comprising 5 μ l of the cDNA pool, 50 pmol Sb4, 50 pmol SBEA1, 5 μ l 5x Taq buffer, 4 μ l 25mM Mg^{2+} , 0.5 μ l 20mM dNTPs, and 1.25u Taq polymerase. All of the reaction components were mixed, before thermocycling at (94°C-45sec, 55°C-30sec, 72°C-1min 30sec) x 30 cycles, followed by a final 10 min extension step at 72°C. Amplification products were separated by electrophoresis through a 1%(w/v) agarose gel and specific amplification products of the predicted size were excised from the gel. The DNA was eluted from the gel slice using QIAGEN's gel extraction kit according to the manufacturers recommendations before ligation with pT7 Blue (Novagen). Ligation was carried out in a 10 μ l reaction volume comprising 7.5 μ l purified amplification product, 1 μ l 10x ligation buffer, 1 μ l pT7Blue and 0.5 μ l T4 DNA ligase (Amersham). The reaction components were mixed well before being placed at 4°C overnight. Following overnight incubation, half of the ligation reaction was used to transform competent Novablue *E. coli* cells (Novagen). Transformed cells were plated out onto LB plates supplemented with X-gal (40 μ gml⁻¹), IPTG (0.1mM), Carbenicillin (100 μ gml⁻¹), and Tetracycline (12.5 μ gml⁻¹), before placing at 37°C overnight. Putative recombinant clones were initially screened for the presence of an insert by colony PCR using the vector specific primers T7B and U19. Insert positive clones were then screened using an insert specific primer in conjunction with either T7B or U19 primers to determine the orientation of the insert within the multiple cloning site prior to sequencing.

Southern blot analysis

Southern analyses of the pre-made nulli-tetra and ditelosomic blots were carried out essentially as described in Jack *et al* (1994).

The SBEII-1 clones discussed above have been cloned into transformation vectors for transformation of wheat.

Northern blot analysis

Northern blots were prepared from total RNA from developing wheat grains of the cultivar Bobwhite. Figure 12 shows a northern blot of RNA from wheat grains of the cultivar Bobwhite grown in the glasshouse as described and harvested between 5 and 29 days after anthesis. The blot was probed with the 1kb SacI SBEII-1 fragment and subsequently (following blot stripping) with the 1.2kb BamHI SBEII-2 fragment, both fragments purified and labelled as described. In Figure 12 panel A shows the Ethidium Bromide-stained RNA gel prior to northern transfer. Panel B shows the results of probing with the SBEII-1 probe and panel C shows the results of probing with the SBEII-2 probe. Comparing within and between panels B and C differences can be observed in the relative intensities of the signals at the different time points. In particular a relatively stronger signal intensity is observed with the SBEII-2 probe for the 5 day time point than with the SBEII-1 probe, indicating that the transcript profiles for SBEII-1 and SBEII-2 are distinct, suggesting that the two gene families (SBEII-1 and SBEII-2) are differentially expressed during grain development. The size of the transcripts observed for both SBEII-1 and SBEII-2 is approximately 3.5kb. However the SBEII-2 transcript is slightly smaller than the SBEII-1 transcript.

Plasmid constructions

Standard molecular biology procedures (Sambrook *et al*, 1989) were used for plasmid constructions.

pWxGS+ (Figure 13) comprising a maize granule bound starch synthase gene (Shure *et al* 1983) promoter-GUS-Nos fusion was obtained as a gift to Unilever Research from Sue Wessler (University of Georgia, Athens, USA) and may be obtained on request from that source. The promoter in pWxGS+ is approximately 1.5kb in length and represents a truncated version of a similar, but larger promoter fragment described in Russell & Fromm (1997). The sequence of the promoter (HindIII - BamHI fragment) in pWxGS+ is presented in Figure 13A (SEQ ID No: 55).

pSRWXGUS1 (Figure 14) was produced by inserting a Sac I linker [d(pCGAGCTCG)0] (New England Biolabs [NEB]) (NEB catalogue No 1044) into the SmaI site in pWxGS+.

pVTWXGUS2 (Figure 15) was produced by inserting a BamHI linker [d(pCGGGATCCCG)] (SEQ ID No: 43) (NEB catalogue No. 1071) into the Eco136II (an isoschizomer of SacI which gives blunt ends) site of pWxGS+.

A SacI linker was inserted at the XbaI site (which had been blunted using Klenow + dNTPs) of the SBEII-1 Clone B6 in the plasmid pT7Blue to produce an intermediate clone. The SBE sequence was then purified from this intermediate clone as a SacI fragment and ligated into the SacI sites of pSRWXGUS1 replacing the GUS gene sequence to produce the plasmids pSR96-26 and pSR96-29 representing antisense and sense orientations of the SBEII-1 sequence downstream of the Waxy promoter, respectively.

A BamHI linker was inserted at the XbaI site (which had been blunted using Klenow + dNTPs) of the SBEII-2 Clone B11 in pT7Blue to produce an intermediate clone. The SBE sequence was then purified from this intermediate as a BamHI fragment and inserted into the BamHI sites of pVTWXGUS2, replacing the GUS gene sequence, to produce the plasmids pVT96-50 and pVT96-53 representing antisense and sense orientations, respectively, of the SBEII-2 sequence downstream of the Waxy promoter.

pVT96-54. A BamHI linker was inserted at the XbaI site (which had been blunted using Klenow + dNTPs) of the SBEII-2 clone B9 (equivalent to clone B1) in pT7Blue to produce an intermediate clone. The SBEII-2 sequence was then purified from this

intermediate clone as a BamHI fragment and inserted into the BamHI sites of pVTWXGUS2, replacing the GUS gene sequence, to produce the plasmid pVT96-54.

The Waxy-SBE-NOS sequences in the plasmids pSR96-26 and pSR96-29 and pVT96-50 and pVT96-53 were purified as HindIII/EcoRI fragments and inserted into the EcoRI/HindIII sites of plasmid pPBI-97-2 (also known as p97-2) (Figure 16). Plasmid pPBI-97-2 is described in European Patent Application No. 97305694.8 (published as WO 99/06570). Following removal of the ampicillin resistance marker gene the resulting plasmids were designated pSR97-26A- (clone B6 (SBEII-1, sub-class A) in antisense orientation), pSR97-29A- (clone B6 in sense orientation), and pSR97-50A- (clone B11 (SBEII-2, sub-class A) in antisense orientation) and pSR97-53A- (clone B11 in sense orientation) as illustrated in Figures 17, 18, 19 and 20, respectively.

p97-2C (Figure 21) was produced by digesting the polylinker sites EcoRI to SmaI in the plasmid pPBI97-2 (Figure 16), ligating and selecting recombinants in which the polylinker region from SmaI to EcoRI had reinserted in the opposite orientation.

The Waxy-NOS sequences in pSRWXGUS1 were transferred as a HindIII/EcoRI fragment into the HindIII/EcoRI sites of plasmid p97-2C to produce the plasmid p97-2CWT1 (Figure 22).

pSC98-1 and pSC98-2. The 5' extended SBEII-1 clone 5A1 in pT7Blue (comprising SBE sequence from coordinate 43 to 2003bp in Figure 10) was digested with EcoRI and XbaI, followed by 'in-fill' of overhangs using Klenow polymerase and dNTPs. The resulting blunt ended SBE fragment was gel purified and ligated to p97-2CWT1 (Figure 22) which had been digested with EcoRI and dephosphorylated using calf intestinal phosphatase. The resulting recombinants were screened by restriction digest analysis and clones comprising both orientations of the SBE sequence (with respect to the waxy promoter) were identified. pSC98-1 (Figure 23) is an antisense version and pSC98-2 (Figure 24) is a sense version. Following removal of the ampicillin marker gene the resulting plasmids were designated pSC98-1A- and pSC98-2A- respectively.

Ubiquitin promoter - NptII selection construct:pUN1

pUN1 was made in the following way:

A SacI linker was inserted at the SmaI site of the plasmid pAHC25 (Christensen and Quail 1996) to produce an intermediate plasmid. The GUS gene was removed from this intermediate plasmid by digesting with SacI followed by self ligation and identification of recombinant molecules lacking the GUS sequence to produce the plasmid pPBI95-9. pPBI95-9 was digested with EcoRI and following self ligation recombinant molecules lacking the Ubi-BAR sequences were identified. The resulting plasmid is designated pPBI96-23. An NptII sequence was amplified as a PCR product using the primers AG95-7:

5'GATGAGCTCCGTTTCGTCATGATTGAACAAGATGG (SEQ ID No: 44) and AG95-8: 5'GTCGAGCTCAGAAGAACTCGTCAAGAAGGC (SEQ ID No: 45), using pPBIBAG3 (Goldsbrough *et al* 1994 as template for the NptII sequence. The amplified product was cloned into the SstI site of pBluescript (Stratagene) and sequenced. The sequencing revealed that the NptII sequence was of the 'mutant' form rather than the wild-type as had been expected. The 'mutant' form carries a single base change which is flanked by unique NcoI and SphI sites. The pBluescript clone was digested with NcoI and SphI to remove the region containing the single base change. Two oligonucleotides, (Npt1:CCCGACGGCGAGGATCTCGTCGTGACC (SEQ ID No: 46) and Npt2: CATGGGTCACGACGAGATCCTCGCCGTCGGGCATG) (SEQ ID No: 47) were then annealed to each other to form an NcoI/SphI fragment. This was cloned into the NcoI/SphI digested Bluescript/NptII clone, and the resulting clone was sequenced to confirm that the gene was now of the wild type form.

The NptII sequences was then purified as a SacI fragment and inserted at the SacI site of pPBI96-23 to produce pUN1 (Figure 25). pUN1 includes the wild-type ubiquitin promoter (Ubi promoter), which is also referred to as the ubiquitin regulatory system (abbreviated to URS). The orientation of the NptII sequence in pUN1 was determined by restriction digest analysis. The sequence of the NptII SacI fragment is presented in Figure 26 (SEQ ID No: 35).

pUSN99-1 and pUSN99-2. The SBEII-1 (clone B6) sequence was purified as a SacI fragment from the plasmid pSR96-26 and inserted at the SacI site of pPBI96-23 to produce the plasmids pUSN99-1 and pUSN99-2 (Figures 27 and 28) representing sense and antisense orientations of the SBEII-1 sequences respectively.

pPBI97-2BdUN1. pPBI92-2BdUN1 (also sometimes referred to as p97-2BdUN1) comprises a reconstituted ubiquitin regulatory system (referred to hereafter as a modified ubiquitin promoter or a modified ubiquitin regulatory system (mURS)) which lacks the two overlapping 'consensus heatshock elements' discussed in EP 0342926 and US 5614399. The modified ubiquitin promoter was prepared via PCR amplification of two DNA fragments using maize genomic DNA as template, followed by ligation of the two fragments to produce a single fragment lacking the consensus heatshock (HS) elements. A KpnI restriction site was engineered in place of the HS elements. The primers used were designed from sequence information published by Liu et al 1995 (EMBL DNA database accession ZMU29159). To delete the HS elements and to replace with a diagnostic KpnI site the ubiquitin promoter and intron sequences were amplified as two fragments using the primer combinations HS1 + Ubi3-3 and HS2 + Ubi5-2, the sequences of which are given below. Primers Ubi5-2 and Ubi3-3 are homologous to sequences in the sequence published by Liu et al 1995. Primers HS1 and HS2 are homologous to sequences located immediately 3' and 5' respectively of the two overlapping HS elements in the ubiquitin promoter as described in EP 0342926 and US 5361399. Both of these primers have a KpnI tail at their 5' ends.

Primers

HS1: 5-ATTAGGTACCGGACTTGCTCCGCTGTCGGC - 3 (SEQ ID No: 48)

HS2: 5-TATAGGTACCGAGGCAGCGACAGAGATGCC -3 (SEQ ID No: 49)

Ubi5-2: 5-AGCTGAATCCGGCGGCATGGC -3 (SEQ ID No: 50)

Ubi3-3: 5-TGATAGTCTTGCCAGTCAGGG -3 (SEQ ID No: 51)

The amplified products were subcloned into pGEM TEasy (Promega) to produce the plasmids p97-U1 and p97-U2. The full-length (approx. 2Kb) modified ubiquitin promoter

was reconstructed by subcloning the KpnI - SacI fragment from p97-U1 into the KpnI/SacI sites of p97-U2 to produce p97-U3. A partial restriction map of the predicted sequence (SEQ ID No: 52) of the cloned fragment in p97-U3 is presented in Figure 29. (The modified ubiquitin promoter (or mURS) is the subject of a copending European Patent Application filed by the present applicants on the same day as the present application, under the reference C1235.01/M). The modified ubiquitin promoter was transferred as a PstI fragment from p97-U3 into plasmid pPBI96-36. The plasmid pPBI96-36 (Figure 30) comprises the GUS-Nos reporter gene fusion under the control of the wild-type ubiquitin promoter (derived from pAHC25) in a pUC plasmid backbone. The promoter replaces the wild-type ubiquitin regulatory system in pPBI96-36 to produce an intermediary plasmid p97-dUG1 (Figure 31).

Construction of pPBI97-2BdUN1

The Ubi-Nos sequences in pPBI96-23 were transferred as an EcoRI - HindIII fragment into the EcoRI and HindIII sites of p97-2B (plasmid p97-2B is described in European Patent Application No. 97305694.8 published as WO 99/06570) to produce the plasmid p97-2BUbiNos. The modified ubiquitin promoter was purified as a HindIII/SacI fragment from p97-dUG1 (Figure 31) and transferred into the HindIII and SacI sites of p97-2BUbiNos, replacing the wild-type ubiquitin promoter to produce p97-2BdUbiNos. The NptII sequence in pUN1 was purified as a SacI fragment and transferred into the SacI site of p97-2BdUbiNos to produce pPBI97-2BdUN1 (Figure 32). Following removal of the ampicillin resistance marker using the method as described in WO 99/06570, the resulting plasmid as used for wheat transformation was designated p97-2BdUN1A-

pCaineo

pCaiNeo comprises the NptII gene under control of a CaMV35S promoter and maize Adh1 intron. The plasmid is described in Fromm et al 1986.

Transformation of wheat

The following plasmid combinations (co-bombardments) have been used in the transformation of wheat plants:

Table 2. Plasmid combinations used in wheat transformation experiments.

Starch gene construct/s	Selection marker construct
	pAHC25
pWXGS+	pUN1
pSR97-26A- antisense	pUN1 or p97-2BdUN1
pSR97-29A- sense	p97-2BdUN1 or pCaiNeo
pSC98-1A- antisense	p97-2BdUN1
pUSN-1 sense	p97-2BdUN1
pUSN-2 antisense	p97-2BdUN1
pUSN-1 sense & pUSN-2 antisense	pUN1
pSC98-2A- sense	p97-2BdUN1

The wheat transformation methods used and described here are largely based on those described by Barcelo and Lazzeri, 1995.

Embryo wheat plants of the spring cultivar Bobwhite and the winter cultivar Florida were grown in a glasshouse with 16hr day length supplemented with lights to maintain a minimum light intensity of $500 \text{ umol m}^{-2}\text{s}^{-1}$ at 0.5M above flag leaf. Glasshouse temperatures were maintained at $19^{\circ}\text{C} \pm 1^{\circ}\text{C}$ during the day and $14^{\circ}\text{C} \pm 1^{\circ}\text{C}$ at night.

Immature embryos of wheat were harvested from developing grain. The seeds were harvested and embryos were cultured at approximately 12 days after anthesis when the embryos were approximately 1mm in length. Seeds were first rinsed in 70% ethanol for 5 minutes and then sterilised in a 10% solution of Domestos bleach (Domestos is a Trade

Mark) for 15 minutes followed by 6 washes with sterile distilled water. Following removal of the embryonic axis the embryos were placed axis surface face down on agar gel (Sigma catalogue no. A-3301) solidified MM1 media. The general recipe for MM1 is given in Appendix 1, and the recipes for the various constituents in Appendix 2. The embryos were maintained in darkness for one to two days at 24°C \pm 1°C prior to bombardment.

The plasmids pAHC25, pCAiNeo, pUN1 and p97-2BdUN1 were used to provide selection markers in the combinations with starch gene constructs as detailed in Table 2. pAHC25 (Christensen and Quail 1996) contains a chimeric Ubi-BAR gene which provides selection of transformants to phosphinothricin, the active ingredient in herbicides BASTA™ and Bialophos (see Block, M.de. *et al* 1987). The plasmids pCAiNeo (Fromm *et al.*, 1986), pUN1 and p97-2BdUN1 contain chimeric promoter-NptII gene fusions and provide selection of transformants against a range of aminoglycoside antibiotics including kanamycin, neomycin, geneticin and paromycin.

Particle bombardments was used to introduce plasmids into plant cells. The following method was used to precipitate plasmid DNA onto 0.6µm gold particles (BIO-RAD catalogue number 165-2262): A total of 5µg of plasmid DNA was added to a 50µl sonicated for one minute suspension of gold particle (@ 10mg/ml) in a 1.5ml microfuge tube. Following a brief vortex for three seconds 50µl of a 0.5M solution of calcium chloride and 20µl of a 0.05M solution of spermidine free base were added to the opposite sides of the microfuge tube lid. The tube contents were mixed together by closing the lid and tapping the calcium chloride and spermidine to the bottom of the tube. Following a vortex for three seconds the suspension was centrifuged at 13,000 rpm for 5 seconds. The supernatant was then removed and the pellet resuspended in 150µl of absolute ethanol. This requires scraping the gold particles off the inside of the tube using a pipette tip. Following a further three second vortex, the sample was centrifuged again and the pellet resuspended in a total volume of 85µl in absolute ethanol. The particles were vortexed briefly and sonicated for 5 seconds in a Camlab Trisonic T310 water bath sonicator to ensure fine dispersion. An aliquot of 5µl of the DNA coated gold particles were placed in the centre of a macrocarrier (BIO-RAD catalogue no. 115-2335) and allowed to dry for

30 mins. Particle bombardment was performed by using a Biolistic™ PDS-1000/He (BIO-RAD Instruments, Hercules CA) chamber which is illustrated schematically in Figure 33, using helium pressure of 650 and 900 psi (rupture discs: BIO-RAD catalogue numbers 165-2327 and 165-2328 respectively).

Referring to Figure 33, the illustrated vacuum chamber comprises a housing 10, the inner side walls of which include a series of recesses 12 for receiving shelves such as sample shelf 14 shown at the fourth level down from the top of the housing. A rupture disc 16 is supported in a He pressure shock tube 18 near the top of the housing. A support 20, resting in the second set of recesses 12 down from the top of the housing, carries unit 22 that includes a stopping screen and a number of rings 24, with 11 rings below the support 20 and 3-4 rings above the support 20. Macrocarrier 26 is supported at the top of unit 22. The approximate distance from the rupture disc 16 to the macrocarrier 26 is 25mm, with the approximate distance from the macrocarrier 26 to the stopping screen being 7mm, and the approximate distance from the stopping screen to the sample shelf 14 being 67mm. The top of unit 22 is about 21mm from the bottom of the shock tube 18, and the bottom unit 22 is about 31mm from the top of sample shelf 14.

Immature embryos were bombarded between 1 and 2 days after culture. For bombardment the immature embryos were grouped into a circular area of approximately 1cm in diameter comprising 20-100 embryos, axis side face down on the MM1 media. The Petri dish (not shown) containing the tissue was placed in the chamber on shelf 14, on the fourth shelf level down from the top, as illustrated in Figure 33. The air in the chamber was then evacuated to a vacuum of 28.5 inches of Hg. The macrocarrier 26 was accelerated with a helium shock wave using rupture membranes that burst when the He pressure in the shock tube 18 reaches 650 or 900 psi. Within 1 hour after bombardment the bombarded embryos were plated on MM1 media at 10 embryos per 9cm petri dish and then maintained in constant darkness at 24°C for 2-3 weeks. During this period somatic embryogenic callus was produced on the bombarded embryos.

After 2-3 weeks the embryos were transferred onto agar-solidified regeneration media, known as R media, and incubated under 16hr daylength at 24°C. The general recipe for

R media is given in Appendix 1. Embryos were transferred on fresh plates at 2-3 week intervals. The composition of the regeneration media varied depending on which selection regime was to be used. For transformants bombarded with the BAR gene the 3 amino solution was omitted and PPT (phosphinothricin) at 1mg/L, rising to 3mg/L over a period of three 2-3 week transfers was used for selection. For selection of transformants using the NptII gene three different regimes were used: 1) Geneticin (GIBCO-BRL catalogue no. 10131-019) was incorporated (at 50mg/L) immediately on transfer to regeneration media and maintained at 50mg/L on subsequent transfers to regeneration media. 2) & 3) Embryos were first transferred to regeneration media without selection for 12 days and 2-3 weeks, respectively, and thereafter transferred on to media containing Geneticin at 50mg/L. After 2-3 passages on regeneration media regenerating shoots were transferred to individual culture tubes containing 15 ml of regeneration media at half salt strength with selection at 3mg/L PPT or 35mg/L geneticin depending on whether the BAR gene or NptII gene had been used in the original bombardments. Following root formation the regenerated plants were transferred to soil and the glasshouse.

Genomic DNA isolation and Southern Analyses

Southern analyses of primary transformants and progeny material were carried out as follows: Freeze dried leaf tissues were ground briefly in a Kontes™ pestle and mortar, and genomic DNA extracted as described in Fulton et al, 1995. 5 µg of DNA were digested with an appropriate restriction enzyme according to the manufacturers instructions, and electrophoresed overnight on a 1% agarose gel, after which the gel was then photographed, washed and blotted onto Hybond N+™ (Amersham International) according to the method of Southern using standard procedures (Sambrook et al 1989). Following blotting, the filters were air dried, baked at 65°C for 1-2 hours and UV fixed at 312nm for 2 minutes.

Probe preparation and labelling for the Southern analyses of transformed material was carried out as described above.

GUS histochemistry was performed essentially as described in Jefferson (1987).

Evaluation of the ubiquitin promoter for constitutive expression of associated transgenes.

The plasmid pAHC25 (Christensen and Quail, 1996) was transformed into wheat as described in previous sections. Transformants were selected on the basis of resistance to phosphinothricin. Southern blot analyses were carried out on the primary transformants to confirm integration of the plasmid sequences (data not shown). GUS histochemical analyses were also carried out and demonstrated that the ubiquitin promoter is capable of mediating high levels of GUS expression in a range of wheat tissues. Figure 34 A, B, C & D show histochemical localisation of GUS expression in the seed, stem, floral and leaf tissues respectively. Southern blot and GUS histochemical analyses were also carried out on self progeny from primary transformants to confirm that the transformation system used is capable of producing transgenic plants which stably transmit the integrated plasmid sequences to progeny plants. Figure 35 shows a Southern blot of 26 progeny plants of transformant BW119 which had been transformed with pAHC25. In this example genomic DNA from the progeny plants was digested with the restriction enzyme SacI and the blot was probed with the GUS gene coding sequence. The Southern blot results are suggestive of the presence of two independently segregating integration loci, each comprising concatamers of pAHC25 plasmid sequences.

Evaluation of the maize waxy promoter for endosperm-specific expression of associated transgenes.

The plasmids pWxGS+ and pUN1 were co-transformed into wheat as described in previous sections. Transformants were selected on the basis of resistance to geneticin. Southern blot analyses were carried out on the primary transformants to confirm integration of the plasmid sequences (data not shown). Gus histochemical analyses were also carried out to determine the expression profile mediated by the maize waxy promoter. The majority of the transformants that expressed GUS exhibited expression specifically in endosperm tissue, demonstrating the suitability of this promoter for mediating endosperm expression of associated transgenes. Figure 36 A & B shows endosperm specific expression of GUS in seeds from two independent transformants. We did not observe GUS expression in pollen grains as was seen by Russell and Fromm (1997), however the

construct they used also incorporated the maize hsp 70 intron which may conceivably have influenced expression both quantitatively and qualitatively.

Transformation of wheat with starch gene constructs.

The various construct combinations detailed in Table 2 were co-transformed into wheat using the procedures as described in previous sections. Transformants were selected on the basis of resistance to geneticin. The primary transformants were confirmed positive by Southern blot analysis. Blots were sequentially probed with an NptII coding sequence probe and a SBE coding region probe. Figure 37 shows an example of a Southern blot which comprises 22 putative transformants which had been co-bombarded with pSR97-29A- or pSR97-26A- and pUN1 or p97-2BdUN1. Genomic DNAs on this blot had been digested with SacI. The blot was first probed with the NptII probe. Lanes marked with an asterisk correspond to transformants which give a positive signal with the NptII probe. The blot shown in Figure 37 was probed with the SBEII-1 1kb SacI fragment. The SacI digest is expected to release a 1kb SBEII-1 hybridising band from both pSR97-29A- and pSR97-26A- plasmid sequences, and the intensity of this band will vary depending on the copy number of inserted plasmid sequences. As can be seen in Figure 37 several additional SBEII-1 hybridising bands are also observed. Five of these bands are present in all lanes and result from hybridisation to endogenous wheat SBEII-1 sequences. The additional bands of varying size which are observed in the majority of lanes which show the 1kb hybridising band most likely result from integration events in which one or more copies of the plasmid had been linearised within the 1kb SBEII-1 sequence prior to integration. In the example shown in Figure 37, of the 20 NptII positive plants, 16 were found to be co-transformed with the SBEII-1 sequences, representing a co-transformation efficiency of 80%.

Differential Scanning Calorimetry (DSC)

When heated, an aqueous suspension of starch in excess water undergoes a co-operative endothermic transition known as gelatinisation, as discussed above, entailing a melting of the starch crystallites. Differential scanning calorimetry (DSC) measures the amount of

energy (heat) absorbed or released by a sample as it is heated, cooled or held in a constant (isothermal) temperature. DSC has been widely used to study the gelatinisation and retrogradation of starch.

DSC analyses were carried out on single grains or pools of 5 grains from primary transformants generated through transformation using each of the gene construct combinations detailed in Table 2.

Two different sample preparation and DSC methodologies were used:

Method 1:

Individual seed samples were crushed and ground using a pestle and mortar. The resulting bran was then separated and samples weighed into 50 μ m aluminium DSC pans. Water, three times by weight, was added and the sample pans sealed. Analyses were performed using a Perkin-Elmer DSC-7 Robotic™ system equipped with an Intercooler II™, for sub-ambient conditions. Samples were heated from 25°C to 80°C at a heating rate of 5°C min⁻¹. Gelatinisation enthalpy, onset and peak and end temperatures were recorded. The thermograms were analysed using the Perkin-Elmer software programs (Thermal Analysis Software 7). Gelatinisation enthalpy is expressed in Joules (J)/gram (g) of sample.

Method 2:

Pools of 5 seeds from a single primary transformant, or single seeds from primary transformants, were milled using a Cemotec 1090™ Sample Mill. The milled sample was then passed through a 250 micron sieve to separate the bran from endosperm. Approximately 5mg of the sieved samples was then accurately weighed into 50 μ l aluminium DSC pans. Water, three times by weight, was added and the sample pans sealed. Analyses were performed using a Perkin-Elmer Pyris 1™ DSC equipped with autosampler and Intracooler IP. Samples were heated from 40°C to 85°C at a heating rate of 10°C per minute. The thermograms were analysed using the Perkin-Elmer software programs (Pyris Software for Windows v 3.5). Gelatinisation enthalpy, onset and peak

and end temperatures were recorded.

Using method 1, DSC analyses were performed on individual mature grains of primary transformants, transformed with the plasmid combinations pSR97-26A-/pUN1, pSR97-26A-/p97-2BdUN1 and pSR97-29A-/p97-2BdUN1. Data obtained were compared to data from control material which had been transformed with one of the NptII selectable marker plasmids, but did not contain any of the 'starch' plasmids. Table 3 summarises the average onset, peak, end and enthalpy values for the selected material. The majority of samples showed similar values to the control material. However, as can be seen from Table 3 onset, peak and end temperatures were higher for a number of the transgenic samples compared to the control material. For example, transformant BW 326 exhibits a 6.7°C, 4.9°C and 4.6°C increase in onset, peak and end temperatures (respectively) compared to the control sample.

Using method 2 a further series of DSC analyses were carried out on pools of 5 grains from primary transformants, transformed with the plasmid combinations pSC98-1A-/p97-2BdUN1, pUSN-1/p97-2BdUN1, pUSN-2/p97-2BdUN1 and pUSN-1/pUSN-2/pUN1. Data obtained were compared to data from control material which had been transformed with one of the NptII selectable marker plasmids, but did not contain any of the 'starch' plasmids. Table 4 summaries the onset, peak, end and enthalpy values for the selected pooled samples. In many cases there is evidence that the 'starch' transgenic material shows onset, peak and end temperatures which are greater than those observed for the control material. For example, transformant BW727 exhibits a 9.8°C, 8.7°C and 9.1°C increase in onset, peak and end temperatures (respectively) compared to the BW control sample 3, and a 7.6°C, 6.8°C and 7.8°C increase in onset, peak and end temperatures (respectively) compared to the BW control sample 2.

Table 3: Results of DSC analyses on single grains using method 1. Data shown are the averages of between 2 and 6 individual grain samples (T_o , T_p and T_f are onset, peak and end temperatures respectively).

Plasmid combination	Line Code	T _o (°C)	T _p (°C)	T _f (°C)	ΔH (J/g)
BW control sample 1		55.2	59.7	66.5	4.66
pSR97-26A-/pUN1	BW283	57.1	60.4	65.0	2.12
	BW135	57.2	62.1	68.6	4.86
	BW324	57.8	62.1	69.1	5.33
	BW325	58.4	61.8	68.7	3.90
	BW326	61.9	64.6	71.1	2.46
	BW348	60.7	63.4	69.7	3.76
pSR97-26A-/p97-2BdUN1	F227	57.4	61.4	67.3	2.65
pSR97-29A-/p97-2BdUN1	F310	62.1	63.7	69.2	6.75
	F312	59.0	62.3	66.8	1.16
	BW335	56.2	60.8	69.1	4.63
	BW353	59.5	62.7	70.8	3.21
	BW354	55.4	61.7	68.9	4.28
	BW355	57.9	61.5	68.0	3.95
	BW357	55.3	60.6	68.0	3.74
	BW363	56.7	62.5	67.9	1.13
	BW367	59.0	62.5	68.2	2.17
	BW369	57.9	60.9	65.9	1.04
	BW370	53.7	59.4	67.5	6.00
	BW375	57.2	61.5	70.0	4.14
	BW376	54.0	58.1	68.0	3.39
	BW377	53.4	60.9	69.2	2.60
	BW380	54.6	61.6	67.6	2.16
	BW390	56.8	61.2	68.5	1.29
	BW399	57.4	62.7	67.9	1.77
	BW400	60.6	63.6	68.1	0.64
	BW341	51.6	59.0	66.4	1.97

Table 4: Results of DSC analyses on pools of 5 grains using method 2. T_o , T_p and T_f are onset, peak and end temperatures respectively

Plasmid combination	Line Code	T_o (°C)	T_p (°C)	T_f (°C)	ΔH (J/g)
F control sample 1		60.1	63.9	68.0	6.30
BW control sample 2		59.3	64.0	68.4	5.94
BW control sample 3		57.08	62.09	67.08	4.28
pSC98-1A-/p97-2BdUN1	BW449	59.3	62.9	67.9	3.95
	BW477	57.7	63.6	70.6	8.30
	F492	62.3	66.4	70.2	7.60
	F494	63.6	67.3	71.0	5.73
	BW511	59.6	63.8	67.2	0.98
	BW518	60.2	64.9	69.2	3.57
	BW519	58.4	63.6	68.5	4.13
	BW527	58.7	63.7	69.0	6.38
	BW549	59.9	64.8	69.3	4.48
	BW550	60.2	64.6	68.9	5.06
	BW552	60.8	62.9	67.9	3.74
	BW553	59.5	63.9	67.5	3.60
	BW555	61.0	66.1	68.2	5.43
	BW557	62.7	66.9	71.0	5.08
	BW559	61.6	65.9	70.8	5.08
	BW563	61.4	65.1	69.4	1.90
	BW564	59.4	64.5	73.2	7.08
	BW576	61.8	65.6	69.3	2.65
	BW587	61.3	65.4	69.4	5.36
	BW614	63.9	67.9	71.8	5.83

	BW618	61.3	65.6	69.7	3.54
	BW583a	58.9	63.7	68.0	3.54
	BW631	61.5	65.6	69.7	4.52
	BW633	61.9	66.0	70.2	5.12
	BW634a	60.8	64.9	70.2	5.10
	BW637a	62.8	67.2	72.0	5.16
	BW639	61.8	65.1	68.9	2.15
	BW640a	62.2	66.7	71.0	3.23
	BW642	63.2	67.2	70.9	4.90
	BW698	62.9	67.0	70.9	4.48
	BW700a	63.8	67.6	71.2	3.41
	BE524a	59.4	64.3	68.9	4.05
pUSN-1/p97-2BdUN1	BW622	59.0	64.1	68.7	4.32
	BW628	56.2	63.3	66.0	6.09
	BW645	57.5	65.6	69.5	5.97
	BW646	61.6	66.4	67.7	3.99
	BW647	61.3	65.4	69.0	3.47
	BW648	59.8	64.4	68.8	4.65
	BW649	61.3	65.6	70.1	5.07
	BW656	59.9	64.6	69.2	5.38
	BW660	62.0	67.3	71.0	4.23
	BW661	61.5	65.8	69.6	3.88
	BW664	61.1	66.1	70.8	4.81
	BW665	61.6	66.5	69.4	5.25
	BW667	63.0	67.1	70.8	3.91
	BW672	63.0	68.1	71.9	5.43
	BW673A	63.1	67.7	71.6	4.83
	BW675	62.1	66.4	71.3	10.97

	BW676	59.8	67.3	71.2	4.21
	BW678	63.0	66.3	69.3	1.20
	BW680	60.8	65.3	70.1	4.94
	BW701	62.3	67.5	72.2	4.70
	BW706	63.0	67.3	71.3	4.94
	BW707	60.9	65.8	70.0	4.77
	BW708	61.7	65.5	68.8	6.11
	BW726	62.6	67.5	71.3	5.44
	BW755	60.8	65.8	70.6	5.18
	BW702	61.9	67.0	71.0	4.44
	BW756	62.3	66.1	69.7	4.83
pUSN-2/p97-2BdUN1	BW625	62.7	68.2	73.8	4.27
	BW653	60.4	65.3	70.1	6.52
	BW704	60.9	66.2	70.2	4.19
	BW718	61.3	66.9	71.2	4.15
	BW719	62.2	67.2	71.7	5.32
	BW722	64.8	67.5	70.0	2.14
	BW740	63.4	67.9	72.3	5.67
	BW741	62.6	66.9	70.5	5.30
	BW742	64.6	67.9	72.0	6.66
	BW752	62.3	66.3	70.0	4.63
pUSN-1/pUSN-2/pUN1	BW685	62.6	65.5	69.0	2.60
	BW686A	61.9	66.3	70.2	4.45
	BW714	63.0	67.6	71.3	3.53
	BW727	66.9	70.8	76.2	5.19
	BW728	62.0	66.3	70.4	5.70
	BW731	63.3	67.9	73.0	4.90

	BW732	63.5	66.8	70.8	4.11
	BW748	62.1	67.4	71.9	5.38
	BW794	62.8	67.5	71.8	5.17

Appendix 1.

Recipe for 2x concentrated MM1 media

Constituent	Volume of stock per litre of 2x concentrated media
Macrosalts MS (10X stock)	200ml
Microsalts L (1000x stock)	2ml
FeNaEDTA MS (100x stock) [Sigma catalogue F-0518]	20ml
Modified Vits MS (x1000)	1ml
3 amino acid solution (25x stock)	40ml
myo inositol (Sigma catalogue number I-3011)	0.2g
sucrose	180g
AgNO ₃ (20mg/ml stock) Added after filter sterilisation	1ml
Picloram (1m/ml stock) Added after filter sterilisation	4ml

Filter sterilise and add to an equal volume of moulten 2x agargel (10g/L).

Recipe for 2x concentrated R media

Constituent	Volume of stock per litre of 2x concentrated media
Macrosalts L7 (10X stock)	200ml
Microsalts L (1000x stock)	2ml
FeNaEDTA MS (100x stock)	20ml
Vits/Inositol L2 (200x stock)	10ml
3 amino acid solution (25x stock)	40ml
Maltose	60g
2,4-D (1mg/ml stock) added after filter sterilisation	200 μ l
Zeatin cis trans mixed isomers (Melford labs catalogue no. Z-0917) (5mg/ml stock) added after filter sterilisation	2ml

Filter sterilise and add to an equal volume of molten 2x agar (16g/litre)

Appendix 2

Recipes for constituents of MM1 and R media

Microsalts L (1000x stock)

	per 100ml
$\text{MnSO}_4 \cdot 7\text{H}_2\text{O}$	1.34g
H_3BO_3	0.5g
$\text{ZnSO}_4 \cdot 7\text{H}_2\text{O}$	0.75g
KI	75mg
$\text{Na}_2\text{MoO}_4 \cdot 2\text{H}_2\text{O}$	25mg
$\text{CuSO}_4 \cdot 5\text{H}_2\text{O}$	2.5mg
$\text{CoCl}_2 \cdot 6\text{H}_2\text{O}$	2.5mg

Filter sterilise through a $22\mu\text{m}$ membrane filter

Store at 4°C

Macrosalts MS (10X stock)

	per litre
NH_4NO_3	16.5g
KNO_3	19.0g
KH_2PO_4	1.7g
$\text{MgSO}_4 \cdot 7\text{H}_2\text{O}$	3.7g
$\text{CaCl}_2 \cdot 2\text{H}_2\text{O}$	4.4g

NB: Dissolve CaCl_2 before mixing with other components

NB: Make up KH_2PO_4 separately in sterile H_2O , and add last.

Store solution at 4°C after autoclaving

Modified MS Vits (1000x stock)

	Per 100ml
Thiamine HCl	10mg
Pyridoxine HCl	50mg
Nicotinic acid	50mg

Store solution in 10ml aliquots at -20°C

3 amino acid solution (25x stock)

	Per litre
L-Glutamine	18.75g
L-Proline	3.75g
L-Asparagine	2.5g

Store solution in 40ml aliquots at -20°C

Macrosalts L7 (10x stock)

	per litre
NH_4NO_3	2.5g
KNO_3	15.0g
KH_2PO_4	2.0g
$\text{MgSO}_4 \cdot 7\text{H}_2\text{O}$	3.5g
$\text{CaCl}_2 \cdot 2\text{H}_2\text{O}$	4.5g

NB: Dissolve CaCl_2 before mixing with other components

NB: Make up KH_2PO_4 separately in 50ml H_2O and add last

Store solution at 4°C after autoclaving

Vits/Inositol (200x stock)

200x Stock	Per 100ml
Inositol	4.0g
Thiamine HCl	0.2g
Pyridoxine HCl	0.02g
Nicotinic acid	0.02g
Ca-pantothenate	0.02g
Ascorbic acid	0.02g

Store solution in 40ml aliquots at -20°C

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Claims

1. A nucleotide sequence encoding substantially the amino acid sequence shown in Figure 10 (SEQ ID No: 2) or a functional equivalent of said nucleotide sequence.
2. A nucleotide sequence comprising substantially the sequence of B2 shown in Figure 3 (SEQ ID No: 3), or a functional equivalent thereof.
3. A nucleotide sequence comprising substantially the sequence of B4 shown in Figure 3 (SEQ ID No: 4), or a functional equivalent thereof.
4. A nucleotide sequence comprising substantially the sequence of B10 shown in Figure 3 (SEQ ID No: 5), or a functional equivalent thereof.
5. A nucleotide sequence comprising substantially the sequence of B1 shown in Figure 3 (SEQ ID No: 6), or a functional equivalent thereof.
6. A nucleotide sequence encoding substantially the amino acid sequence of B6 shown in Figure 4 (SEQ ID No: 7), or a functional equivalent thereof.
7. A portion of any of the above sequences, comprising at least 500 base pairs and having at least 90% sequence homology to the corresponding portion of the sequence from which it is derived.
8. A nucleotide sequence comprising substantially the sequence shown in Figure 5 (SEQ ID No: 8), Figure 6 (SEQ ID No: 9) or Figure 7 (SEQ ID No: 10), or a functional equivalent thereof.
9. A nucleic acid construct comprising a nucleotide sequence in accordance with any of the preceding claims.

10. A construct according to claim 9, wherein the sequence is operably linked, in sense or antisense orientation, to a promoter sequence.
11. An expression vector comprising a construct according to claim 9 or 10.
12. A host cell into which has been introduced a sequence, construct or vector in accordance with anyone of the preceding claims.
13. An amino acid sequence encoded by the nucleotide sequence of anyone of claims 1 to 8.
14. A method of altering the characteristics of a plant, comprising introducing into the plant the sequence of any one of claims 1 to 11 operably linked to a suitable promoter active in the plant so as to affect expression of a gene present in the plant.
15. A method according to claim 14, wherein the sequence is linked in the antisense orientation to the promoter.
16. A method according to claim 14 or 15, wherein the plant is a wheat plant.
17. A method according to claim 14, 15 or 16, wherein the characteristic altered relates to the starch content and/or starch composition of the plant.
18. A plant or plant cell having characteristics altered by the method of any one of claims 14 to 17, or the progeny of such a plant or part of such a plant.
19. A plant, plant cell, progeny or part thereof according to claim 18, wherein the plant is a wheat plant.
20. A storage organ from a plant according to claim 18 or 19.
21. A plant, plant cell, progeny or part thereof according to any one of claims 18 to 20,

containing starch having an elevated gelatinisation onset and/or peak temperature as measured by DSC compared to starch from a similar, but unaltered, plant.

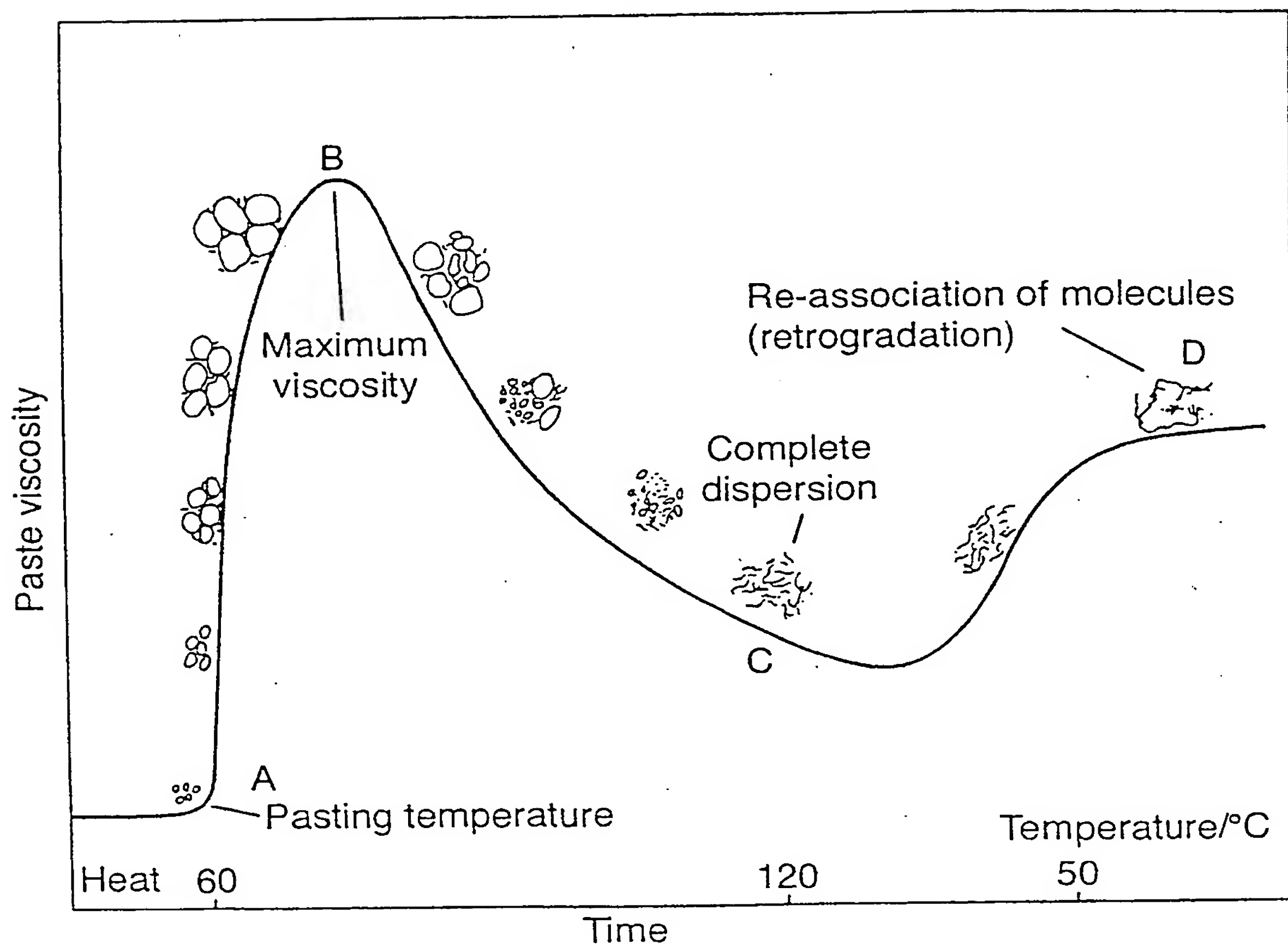
22. Starch obtainable or obtained from a plant in accordance with any one of claims 18 to 21.

23. A method of making altered starch, comprising altering a plant by the method of any one of claims 14 to 17, and extracting therefrom starch having altered properties compared to starch extracted from equivalent, but unaltered, plants.

24. Use of starch according to claim 22 in the preparation of processing of a foodstuff, particularly bakery products.

25. A foodstuff, particularly a bakery product, comprising starch in accordance with claim 22.

Fig.1.



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Fig. 2(ii).

44	DYRYS	EYRR	IRAA	IDQ	HEGGLE	AFSR	GYEK	LGFT	IRSA	EGIT	TYRE	WAP	GAH	SAAL	VGD	FNN	OsbeII-1ALL	
628	DYRYS	EYRR	IRAA	IDQ	HEGGLE	AFSR	GYEK	LGFT	IRSA	EGIT	TYRE	WAP	GAH	SAAL	VGD	FNN	Wheat SBEII-2	
440	EYRYS	LYRR	IRSD	IDQ	HEGGLE	AFSR	SYEK	FGFN	ASAE	GIT	TYRE	WAP	GAH	SAAL	VGD	FNN	ZMSBE2a	
496	EYRYS	LYRR	IRSD	IDQ	HEGGLE	AFSR	SYEK	FGFN	ASAE	GIT	TYRE	WAP	GAH	SAAL	VGD	FNN	ZMSBE2b	
2																	Barley SBEIIa	
2																	Barley SBEIIb	
611	EYRYS	LYRR	LRSD	IDQ	HEGGLE	TFSR	GYEK	KFGFN	SAEG	VYTY	REW	APGAH	SAAL	VGD	FNN	RICBCE3		
611	EYRYS	LYRR	LRSD	IDQ	HEGGLE	TFSR	GYEK	KFGFN	SAEG	VYTY	REW	APGAH	SAAL	VGD	FNN	RICESBE-1/97		
766	DYRYS	LYRR	IRSD	IDQ	HEGGLE	AFSR	GYEK	KFGFN	ASAE	GIT	TYRE	WAP	GAH	SAAL	VGD	FNN	PSSBEIGEN	
457	RHR	HKRY	QKHL	IEK	HEGGLE	AFSR	GYEK	KFGFN	ASAE	GIT	TYRE	WAP	GAH	SAAL	VGD	FNN	STSE	
304	SYR	HKRY	QKHL	IEK	HEGGLE	AFSR	GYEK	KFGFN	ASAE	GIT	TYRE	WAP	GAH	SAAL	VGD	FNN	TASBEI	
331	DYRYS	LYRR	LRSD	IDQ	HEGGLE	AFSR	GYEK	KFGFN	ASAE	GIT	TYRE	WAP	GAH	SAAL	VGD	FNN	TASBE1D2	
311	RHR	HKRY	QKHL	IEK	HEGGLE	AFSR	GYEK	KFGFN	ASAE	GIT	TYRE	WAP	GAH	SAAL	VGD	FNN	ZMSBEI	
296	HYR	IKRY	QKHL	IEK	HEGGLE	AFSR	GYEK	KFGFN	ASAE	GIT	TYRE	WAP	GAH	SAAL	VGD	FNN	RICBEI	
292	KYR	LKRY	QKHL	IEK	HEGGLE	AFSR	GYEK	KFGFN	ASAE	GIT	TYRE	WAP	GAH	SAAL	VGD	FNN	PSSBEIIGH	
44	WNPN	NADRM	SKNE	FGV	WVE	IFLP	NNAD	GSPP	IPHG	SRVK	VVRM	DTSP	SGVI	KDS	IPAW	IKY	OsbeII-1ALL	
808	WNPN	NADRM	SKNE	FGV	WVE	IFLP	NNAD	GSPP	IPHG	SRVK	VVRM	DTSP	SGVI	KDS	IPAW	IKY	Wheat SBEII-2	
620	WNPN	NADRM	SKNE	FGV	WVE	IFLP	NNAD	GSPP	IPHG	SRVK	VVRM	DTSP	SGVI	KDS	IPAW	IKY	ZMSBE2a	
676	WNPN	NADRM	SKNE	FGV	WVE	IFLP	NNAD	GSPP	IPHG	SRVK	VVRM	DTSP	SGVI	KDS	IPAW	IKY	ZMSBE2b	
2																	Barley SBEIIa	
2																	Barley SBEIIb	
791	WNPN	NADRM	SKNE	FGV	WVE	IFLP	NNAD	GSPP	IPHG	SRVK	VVRM	DTSP	SGVI	KDS	IPAW	IKY	RICBCE3	
791	WNPN	NADRM	SKNE	FGV	WVE	IFLP	NNAD	GSPP	IPHG	SRVK	VVRM	DTSP	SGVI	KDS	IPAW	IKY	RICESBE-1/97	
946	WNPN	NADRM	SKNE	FGV	WVE	IFLP	NNAD	GSPP	IPHG	SRVK	VVRM	DTSP	SGVI	KDS	IPAW	IKY	PSSBEIGEN	
637	WNG	SNHMM	TKDN	YGV	WVS	IRIP	DO -	VDSK	PPV	IPHN	SRVK	FHGR	GVW	VVD	IPAW	IKY	STSE	
484	WNG	SGHRM	TKDN	YGV	WVS	IRIP	SH -	VNGK	PPA	IPHN	SRVK	FHGR	GVW	VVD	IPAW	IKY	TASBEI	
511	WNG	SGHRM	TKDN	YGV	WVS	IRIP	SH -	VNGK	PPA	IPHN	SRVK	FHGR	GVW	VVD	IPAW	IKY	TASBE1D2	
491	WNG	SGHRM	TKDN	YGV	WVS	IRIP	SH -	VNGK	PPA	IPHN	SRVK	FHGR	GVW	VVD	IPAW	IKY	ZMSBEI	
476	WNG	SGHRM	TKDN	YGV	WVS	IRIP	SH -	VNGK	PPA	IPHN	SRVK	FHGR	GVW	VVD	IPAW	IKY	RICBEI	
472	WNG	SGHRM	TKDN	YGV	WVS	IRIP	SH -	VNGK	PPA	IPHN	SRVK	FHGR	GVW	VVD	IPAW	IKY	PSSBEIIGH	
185	TPG	GI	YV	DD	PP	EE	EK	YV	FK	HP	QPK	RRPK	SLRI	YE	TH	VG	MS	OsbeII-1ALL
985	APG	GI	YV	DD	PP	EE	EK	YV	FK	HP	QPK	RRPK	SLRI	YE	TH	VG	MS	Wheat SBEII-2
797	APG	GI	YV	DD	PP	EE	EK	YV	FK	HP	QPK	RRPK	SLRI	YE	TH	VG	MS	ZMSBE2a
853	APG	GI	YV	DD	PP	EE	EK	YV	FK	HP	QPK	RRPK	SLRI	YE	TH	VG	MS	ZMSBE2b
149																	Barley SBEIIa	
149																	Barley SBEIIb	
968	APG	GI	YV	DD	PP	EE	EK	YV	FK	HP	QPK	RRPK	SLRI	YE	TH	VG	MS	RICBCE3
968	APG	GI	YV	DD	PP	EE	EK	YV	FK	HP	QPK	RRPK	SLRI	YE	TH	VG	MS	RICESBE-1/97
1123	APG	GI	YV	DD	PP	EE	EK	YV	FK	HP	QPK	RRPK	SLRI	YE	TH	VG	MS	PSSBEIGEN
814	ATK	FA	APY	DD	PP	PP	SS	ERY	VV	FK	HP	QPK	RRPK	SLRI	YE	TH	VG	STSE
661	ATK	FA	APY	DD	PP	PP	SS	ERY	VV	FK	HP	QPK	RRPK	SLRI	YE	TH	VG	TASBEI
685	TASE	SG	APY	DD	PP	PP	SS	ERY	VV	FK	HP	QPK	RRPK	SLRI	YE	TH	VG	TASBE1D2
665	DASE	SG	APY	DD	PP	PP	SS	ERY	VV	FK	HP	QPK	RRPK	SLRI	YE	TH	VG	ZMSBEI
653	DASE	SG	APY	DD	PP	PP	SS	ERY	VV	FK	HP	QPK	RRPK	SLRI	YE	TH	VG	RICBEI
649	DPT	TR	FA	APY	DD	PP	PP	SS	ERY	VV	FK	HP	QPK	RRPK	SLRI	YE	TH	PSSBEIIGH

Fig. 2(iii)

359	VLPRIK	R	L	G	N	A	V	Q	I	M	A	I	Q	E	H	S	Y	Y	G	S	F	G	Y	H	V	T	N	-	F	F	A	P	S	S	R	F	G	S	P	E	D	L	K	S	L	I	D	R	A	H	E	L	G	L	OsbeII-1ALL	
1159	VLPRIK	R	L	G	N	A	V	Q	I	M	A	I	Q	E	H	S	Y	Y	A	S	F	G	Y	H	V	T	N	-	F	F	A	P	S	S	R	F	G	T	P	E	D	L	K	S	L	I	D	R	A	H	E	L	G	L	Wheat SBEII-2	
971	VLPRIK	R	L	G	N	A	V	Q	I	M	A	I	Q	E	H	S	Y	Y	A	S	F	G	Y	H	V	T	N	-	F	F	A	P	S	S	R	F	G	T	P	E	D	L	K	S	L	I	D	R	A	H	E	L	G	L	ZMSBE2a	
1027	VLPRIK	R	L	G	N	A	V	Q	I	M	A	I	Q	E	H	S	Y	Y	G	S	F	G	Y	H	V	T	N	-	F	F	A	P	S	S	R	F	G	T	P	E	D	L	K	S	L	I	D	R	A	H	E	L	G	L	ZMSBE2b	
149																																																	Barley SBEIIa							
149																																																	Barley SBEIIb							
1142	VLPRIK	K	L	G	N	A	V	Q	I	M	A	I	Q	E	H	A	Y	Y	G	S	F	G	Y	H	V	T	N	-	F	F	A	P	S	S	R	F	G	T	P	E	D	L	K	S	L	I	D	K	A	H	E	L	G	L	RICCE3	
1142	VLPRIK	K	L	G	N	A	V	Q	I	M	A	I	Q	E	H	A	Y	Y	G	S	F	G	Y	H	V	T	N	-	F	F	A	P	S	S	R	F	G	T	P	E	D	L	K	S	L	I	D	K	A	H	E	L	G	L	RICESBE-1/97	
1297	VLPRIK	K	L	G	N	A	V	Q	I	M	A	I	Q	E	H	S	Y	Y	A	S	F	G	Y	H	V	T	N	-	F	F	A	P	S	S	R	F	G	T	P	E	D	L	K	S	L	I	D	K	A	H	E	L	G	L	PSSEIEN	
994	VLPRIK	K	L	G	N	A	V	Q	I	M	A	I	Q	E	H	S	Y	Y	G	S	F	G	Y	H	V	T	N	-	F	F	A	P	S	S	R	F	G	T	P	E	D	L	K	S	L	I	D	K	A	H	S	L	G	L	STSBE	
841	VLPRIK	K	L	G	N	A	V	Q	I	M	A	I	Q	E	H	S	Y	Y	A	S	F	G	Y	H	V	T	N	-	F	F	A	P	S	S	R	F	G	T	P	E	D	L	K	S	L	I	D	K	A	H	S	L	G	L	TASBEI	
865	VLPRIK	K	L	G	N	A	V	Q	I	M	A	I	Q	E	H	S	Y	Y	A	S	F	G	Y	H	V	T	N	-	F	F	A	P	S	S	R	F	G	T	P	E	D	L	K	S	L	I	D	K	A	H	S	L	G	L	TASBE102	
845	VLPRIK	K	L	G	N	A	V	Q	I	M	A	I	Q	E	H	S	Y	Y	A	S	F	G	Y	H	V	T	N	-	F	F	A	P	S	S	R	F	G	T	P	E	D	L	K	S	L	I	D	K	A	H	S	L	G	L	ZMSBEI	
833	VLPRIK	K	L	G	N	A	V	Q	I	M	A	I	Q	E	H	S	Y	Y	A	S	F	G	Y	H	V	T	N	-	F	F	A	P	S	S	R	F	G	T	P	E	D	L	K	S	L	I	D	K	A	H	S	L	G	L	RICBEI	
829	VLPRIK	K	L	G	N	A	V	Q	I	M	A	I	Q	E	H	S	Y	Y	A	S	F	G	Y	H	V	T	N	-	F	F	A	P	S	S	R	F	G	T	P	E	D	L	K	S	L	I	D	K	A	H	S	L	G	L	PSSEIIGN	
536	VLMDOV	V	V	H	S	H	A	S	N	N	T	L	D	G	L	N	G	F	D	-	-	G	T	D	T	H	Y	F	H	G	G	S	R	G	H	H	W	M	W	D	S	R	L	F	N	Y	G	N	K	E	V	I	R	F	L	OsbeII-1ALL
1336	VLMDOV	V	V	H	S	H	A	S	N	N	T	L	D	G	L	N	G	F	D	-	-	G	T	D	T	H	Y	F	H	G	G	S	R	G	H	H	W	M	W	D	S	R	L	F	N	Y	G	N	K	E	V	I	R	F	L	Wheat SBEII-2
1148	VLMDOV	V	V	H	S	H	A	S	N	N	T	L	D	G	L	N	G	F	D	-	-	G	T	D	T	H	Y	F	H	G	G	S	R	G	H	H	W	M	W	D	S	R	L	F	N	Y	G	N	K	E	V	I	R	F	L	ZMSBE2a
1204	VLMDOV	V	V	H	S	H	A	S	N	N	T	L	D	G	L	N	G	F	D	-	-	G	T	D	T	H	Y	F	H	G	G	S	R	G	H	H	W	M	W	D	S	R	L	F	N	Y	G	N	K	E	V	I	R	F	L	ZMSBE2b
149																																																	Barley SBEIIa							
149																																																	Barley SBEIIb							
1319	VLMDOV	V	V	H	S	H	A	S	N	N	T	L	D	G	L	N	G	F	D	-	-	G	T	D	T	H	Y	F	H	G	G	S	R	G	H	H	W	M	W	D	S	R	L	F	N	Y	G	N	K	E	V	I	R	F	L	RICCE3
1319	VLMDOV	V	V	H	S	H	A	S	N	N	T	L	D	G	L	N	G	F	D	-	-	G	T	D	T	H	Y	F	H	G	G	S	R	G	H	H	W	M	W	D	S	R	L	F	N	Y	G	N	K	E	V	I	R	F	L	RICESBE-1/97
1474	VLMDOV	V	V	H	S	H	A	S	N	N	T	L	D	G	L	N	G	F	D	-	-	G	T	D	T	H	Y	F	H	G	G	S	R	G	H	H	W	M	W	D	S	R	L	F	N	Y	G	N	K	E	V	I	R	F	L	PSSEIEN
1171	VLMDOV	V	V	H	S	H	A	S	N	N	T	L	D	G	L	N	G	F	D	-	-	G	T	D	T	H	Y	F	H	G	G	S	R	G	H	H	W	M	W	D	S	R	L	F	N	Y	G	N	K	E	V	I	R	F	L	STSBE
1018	VLMDOV	V	V	H	S	H	A	S	N	N	T	L	D	G	L	N	G	F	D	-	-	G	T	D	T	H	Y	F	H	G	G	S	R	G	H	H	W	M	W	D	S	R	L	F	N	Y	G	N	K	E	V	I	R	F	L	TASBEI
1042	VLMDOV	V	V	H	S	H	A	S	N	N	T	L	D	G	L	N	G	F	D	-	-	G	T	D	T	H	Y	F	H	G	G	S	R	G	H	H	W	M	W	D	S	R	L	F	N	Y	G	N	K	E	V	I	R	F	L	TASBE102
1022	VLMDOV	V	V	H	S	H	A	S	N	N	T	L	D	G	L	N	G	F	D	-	-	G	T	D	T	H	Y	F	H	G	G	S	R	G	H	H	W	M	W	D	S	R	L	F	N	Y	G	N	K	E	V	I	R	F	L	ZMSBEI
1010	VLMDOV	V	V	H	S	H	A	S	N	N	T	L	D	G	L	N	G	F	D	-	-	G	T	D	T	H	Y	F	H	G	G	S	R	G	H	H	W	M	W	D	S	R	L	F	N	Y	G	N	K	E	V	I	R	F	L	RICBEI
1009	VLMDOV	V	V	H	S	H	A	S	N	N	T	L	D	G	L	N	G	F	D	-	-	G	T	D	T	H	Y	F	H	G	G	S	R	G	H	H	W	M	W	D	S	R	L	F	N	Y	G	N	K	E	V	I	R	F	L	PSSEIIGN
707	LSNARW	W	L	E	E	Y	K	F	D	G	F	R	F	D	G	A	T	S	M	M	Y	T	H	H	G	L	Q	V	A	F	T	G	N	Y	S	E	Y	F	G	F	A	T	D	V	D	A	V	Y	L	M	L	M	N	D	OsbeII-1ALL	
1507	LSNARW	W	L	E	E	Y	K	F	D	G	F	R	F	D	G	A	T	S	M	M	Y	T	H	H	G	L	Q	V	A	F	T	G	N	Y	S	E	Y	F	G	F	A	T	D	V	D	A	V	Y	L	M	L	M	N	D	Wheat SBEII-2	
1319	LSNARW	W	L	E	E	Y	K	F	D	G	F	R	F	D	G	A	T	S	M	M	Y	T	H	H	G	L	Q	V	A	F	T	G	N	Y	S	E	Y	F	G	F	A	T	D	V	D	A	V	Y	L	M	L	M	N	D	ZMSBE2a	
1375	LSNARW	W	L	E	E	Y	K	F	D	G	F	R	F	D	G	A	T	S	M	M	Y	T	H	H	G	L	Q	V	A	F	T	G	N	Y	S	E	Y	F	G	F	A	T	D	V	D	A	V	Y	L	M	L	M	N	D	ZMSBE2b	
149																																																	Barley SBEIIa							
149																																																	Barley SBEIIb							
1490	LSNARW	W	L	E	E	Y	K	F	D	G	F	R	F	D	G	A	T	S	M	M	Y	T	H	H	G	L	Q	V	A	F	T	G	N	Y	S	E	Y	F	G	F	A	T	D	V	D	A	V	Y	L	M	L	M	N	D	RICCE3	
1490	LSNARW	W	L	E	E	Y	K	F	D	G	F	R	F	D	G	A	T	S	M	M	Y	T	H	H	G	L	Q	V	A	F	T	G	N	Y	S	E	Y	F	G	F	A	T	D	V	D	A	V	Y	L	M	L	M	N	D	RICESBE-1/97	
1645	LSNARW	W	L	E	E	Y	K	F	D	G	F	R	F	D	G	A	T	S	M	M	Y	T	H	H	G	L	Q	V	A	F	T	G	N	Y	S	E	Y	F	G	F	A	T	D	V	D	A	V	Y	L	M	L	M	N	D	PSSEIEN	
1351	LSNARW	W	L	E	E	Y	K	F	D	G	F	R	F	D	G	A	T	S	M	M	Y	T	H	H	G	L	Q	V	A	F	T	G	N	Y	S	E	Y	F	G	F	A	T	D	V	D	A	V	Y	L	M	L	M	N	D	STSBE	
1198	LSNARW	W	L	E	E	Y	K	F	D	G	F	R	F	D	G	A	T	S	M	M	Y	T	H	H	G	L	Q	V	A	F	T	G	N	Y	S	E	Y	F	G	F	A	T	D	V	D	A	V	Y	L	M	L	M	N	D	TASBEI	
1222	LSNARW	W	L	E	E	Y	K	F	D	G	F	R	F	D	G	A	T	S	M	M	Y	T	H	H	G	L	Q	V	A	F	T	G	N	Y	S	E	Y	F	G	F	A	T	D	V	D	A	V	Y	L	M	L	M	N	D	TASBE102	
1202	LSNARW																																																							

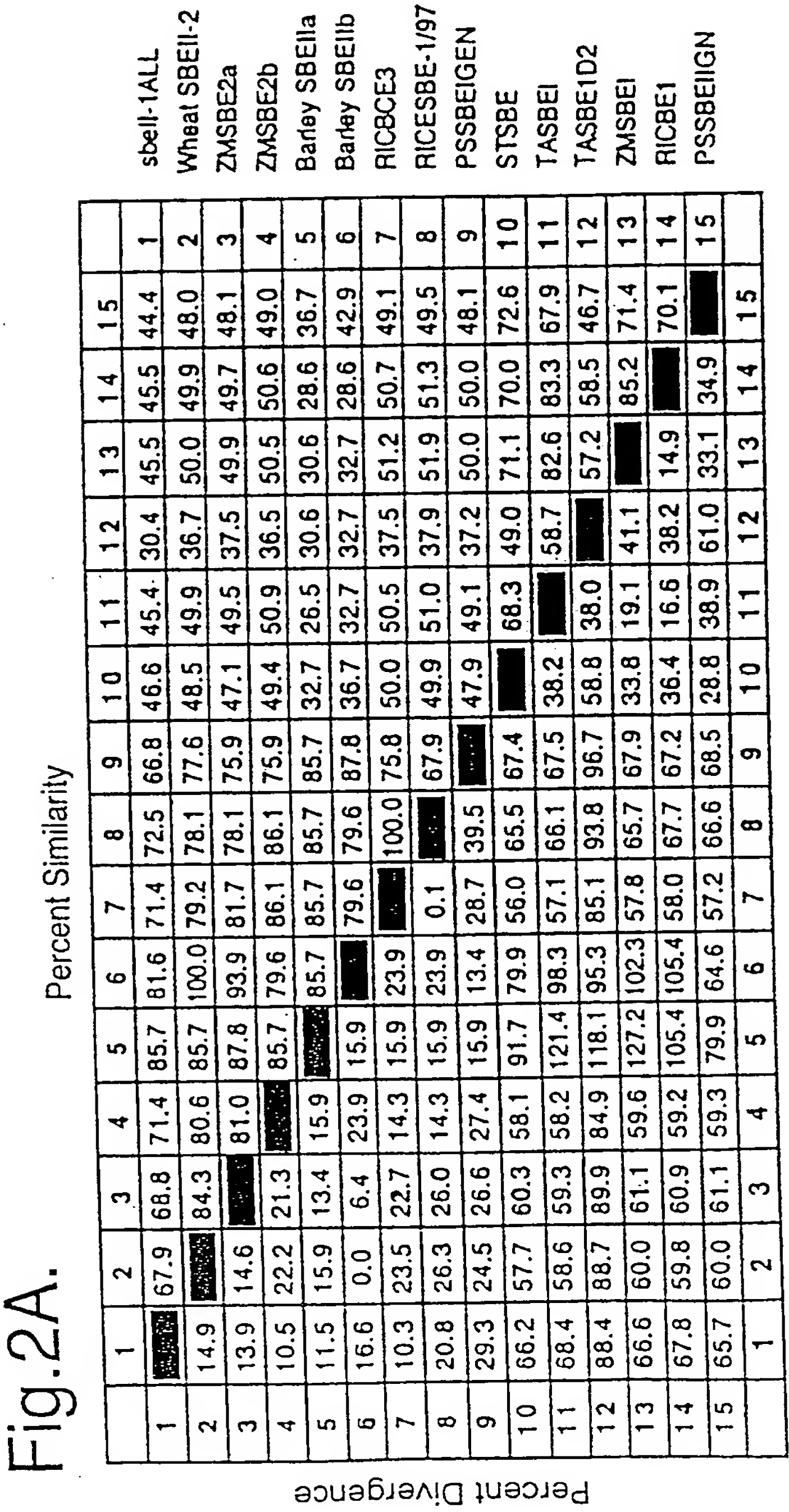
Fig. 2(iv)

1887	L I H G F Y P E A V T I G E D V S G M P T F A L P V Q D G G V G F D Y R L H M A V A D K W I E L L K - G N D E A W E M G	O s b e i l - 1 A L L
1867	L I H G L H P O A V S I G E D V S G M P T F C I P V P D G G V G L D Y R L H M A V A D K W I E L L K - Q S D E S W K M G	W h e a t S B E I I - 2
1499	L I R G L Y P E A V S I G E D V S G M P T F C I P V Q O G G V G F D Y R L H M A V P D K W I E L L K - Q S D E Y W E M G	Z M S B E 2 a
1555	L I H G L Y P E A V T I G E D V S G M P T F A L P V H D G G V G F D Y R L H M A V A D K W I D L L K - Q S D E T W K M G	Z M S B E 2 b
149		B a r l e y S B E I I a
149		B a r l e y S B E I I b
1670	L I H G L Y P E A I T I G E D V S G M P T F A L P V Q D G G V G F D Y R L H M A V P D K W I E L L K - Q S D E S W K M G	R I C B C E 3
1670	L I H G L Y P E A I T I G E D V S G M P T F A L P V Q D G G V G F D Y R L H M A V P D K W I E L L K - Q S D E S W K M G	R I C E S B E - 1 / 97
1825	L I H G L F P E A V S I G E D V S G M P T F C L P T Q D G G V G F M Y R L H M A V A D K W I E L L K - K Q D E D W R M G	P S S B E I G E N
1531	L I H X I F P D A T V I A E D V S G M P G L G R P V S E G G I G F D Y R L H M A I P D K W I D Y L K N K N D E D W S M K	S T S B E
1378	L M H K L L P E A T V V A E D V S G M P V L C R S V D E G G V G F D Y R L H M A I P D R W I D Y L K N K D D L E W S M S	T A S B E I
1402	L M H K L L P E A I V V A E D V S G M P V L C W P V D E G G L G F D Y R Q A M I I P D R W I D Y L K N K G D Q Q W S M S	T A S B E I D 2
1382	L M H K L L P E A T V V A E D V S G M P V L C R P V D E G G V G F D Y R L H M A I P D R W I D Y L K N K D D S E W S M G	Z M S B E I
1370	L M H K L L P E A T V V A E D V S G M P V L C R P V D E G G V G F D E R L H M A I P D R W I D Y L K N K E D R K W S M S	R I C B E I
1366	L V H O I L P D A T O I A E D V S G M P G L G R P V S E V G I G F D Y R L H M A I P D K W I D Y L K N K K D S E W S M K	P S S B E I I G N
1064	N I V - H T L T N R R W P E K C V T Y A E S H D Q Q A L V G D K T I A F W L M D K D M Y D F M A L N G P S T P S I D R G I	O s b e i l - 1 A L L
1864	D I V - H T L T N R R W L E K C V T Y A E S H D Q Q A L V G D K T I A F W L M D K D M Y D F M A L D R P S T P R I D R G I	W h e a t S B E I I - 2
1676	D I V - H T L T N R R W L E K C V T Y C E S H D Q Q A L V G D K T I A F W L M D K D M Y D F M A L D R P S T P R I D R G I	Z M S B E 2 a
1732	D I V - H T L T N R R W L E K C V T Y A E S H D Q Q A L V G D K T I A F W L M D K D M Y D F M A L D R P S T P T I D R G I	Z M S B E 2 b
149		B a r l e y S B E I I a
149		B a r l e y S B E I I b
1847	D I V - H T L T N R R W S E K C V T Y A E S H D Q Q A L V G D K T I A F W L M D K D M Y D F M A L D R P A T P S I D R G I	R I C B C E 3
1847	D I V - H T L T N R R W S E K C V T Y A E S H D Q Q A L V G D K T I A F W L M D K D M Y D F M A L D R P A T P S I D R G I	R I C E S B E - 1 / 97
2002	D I V - H T L T N R R W L E K C V V Y A E S H D Q Q A L V G D K T I A F W L M D K D M Y D F M A L D R P S I D R G I	P S S B E I G E N
1711	E - V T S S L T N R R Y T E K C I A Y A E S H D Q S I V G D K T I A F L L M D K E M Y S G M S C L T D A S P Y V D R G I	S T S B E
1558	G - I A H T L T N R R Y T E K C I A Y A E S H D Q S I V G D K T I A F L L M D K E M Y T G M S D L Q P A S P T I D R G I	T A S B E I
1582	S V I S O T L T N R R Y T E K F I A Y A E R O N H S I I G S K T I A F L L M E E T Y S G M S A M D P D S P T I D R A I	T A S B E I D 2
1562	E - I A H T L T N R R Y T E K C I A Y A E S H D Q S I V G D K T I A F L L M D K E M Y T G M S D L Q P A S P T I D R G I	Z M S B E I
1550	E - I V Q T L T N R R Y T E K C I A Y A E S H D Q S I V G D K T I A F L L M D K E M Y T G M S D L Q P A S P T I M R G I	R I C B E I
1546	E - I S L H T N R R Y T E K C V S Y A E S H D Q S I V G D K T I A F L L M D E E M Y S S M S C L T M L S P T I E R G I	P S S B E I I G N
1241	A L H K M I R L I T M G L G G E G Y L N F M G N E F G H P E W I D F P R G P Q V L P T G K F I P G N N N S Y D K C R - R	O s b e i l - 1 A L L
2041	A L H K M I R L V T M G L G G E G Y L N F M G N E F G H P E W I D F P R G P Q T L P T G K V L P G N N N S Y D K C R - R	W h e a t S B E I I - 2
1853	A L H K M I R L V T M G L G G E G Y L N F M G N E F G H P E W I D F P R G P Q S L P N G S V I P G N N N S Y D K C R - R	Z M S B E 2 a
1909	A L H K M I R L I T M G L G G E G Y L N F M G N E F G H P E W I D F P R G P Q R L P S G K F I P G N N N S Y D K C R - R	Z M S B E 2 b
149		B a r l e y S B E I I a
149		B a r l e y S B E I I b
2024	A L H K M I R L I T M G L G G E G Y L N F M G N E F G H P E W I D F P R A P Q V L P N G K F I P G N N N S Y D K C R - R	R I C B C E 3
2024	A L H K M I R L I T M G L G G E G Y L N F M G N E F G H P E W I D F P R A P Q V L P N G K F I P G N N N S Y D K C R - R	R I C E S B E - 1 / 97
2179	A L H K M I R L I T M G L G G E G Y L N F M G N E F G H P E W I D F P R G E O H L P N G K I V P G N N N S Y D K C R - R	P S S B E I G E N
1888	A L H K M I H F F I T M A L G G E G Y L N F M G N E F G H P E W I D F P R E - - - - - G N N W S Y D K C R - R	S T S B E
1735	A L Q K M I H F F I T M A L G G D G Y L N F M G N E F G H P E W I D F P R E - - - - - G N N W S Y D K C R - R	T A S B E I
1762	A L Q K M I H F F I T M A L F G G D S Y L K F M G N E -	T A S B E I D 2
1739	A L Q K M I H F F I T M A L G G D G Y L N F M G N E F G H P E W I D F P R E - - - - - G N N W S Y D K C R - R	Z M S B E I
1727	A L Q K M I H F F I T M A L G G D G Y L N F M G N E F G H P E W I D F P R E - - - - - G N N W S Y D K C R - R	R I C B E I
1723	S U H K M I H F I T L A L G G E G Y L N F M G N E F G H P E W I D F P R E - - - - - G N G W S Y E K C R L T P S S B E I I G N	P S S B E I I G N

Fig. 2(v)

[illegible]

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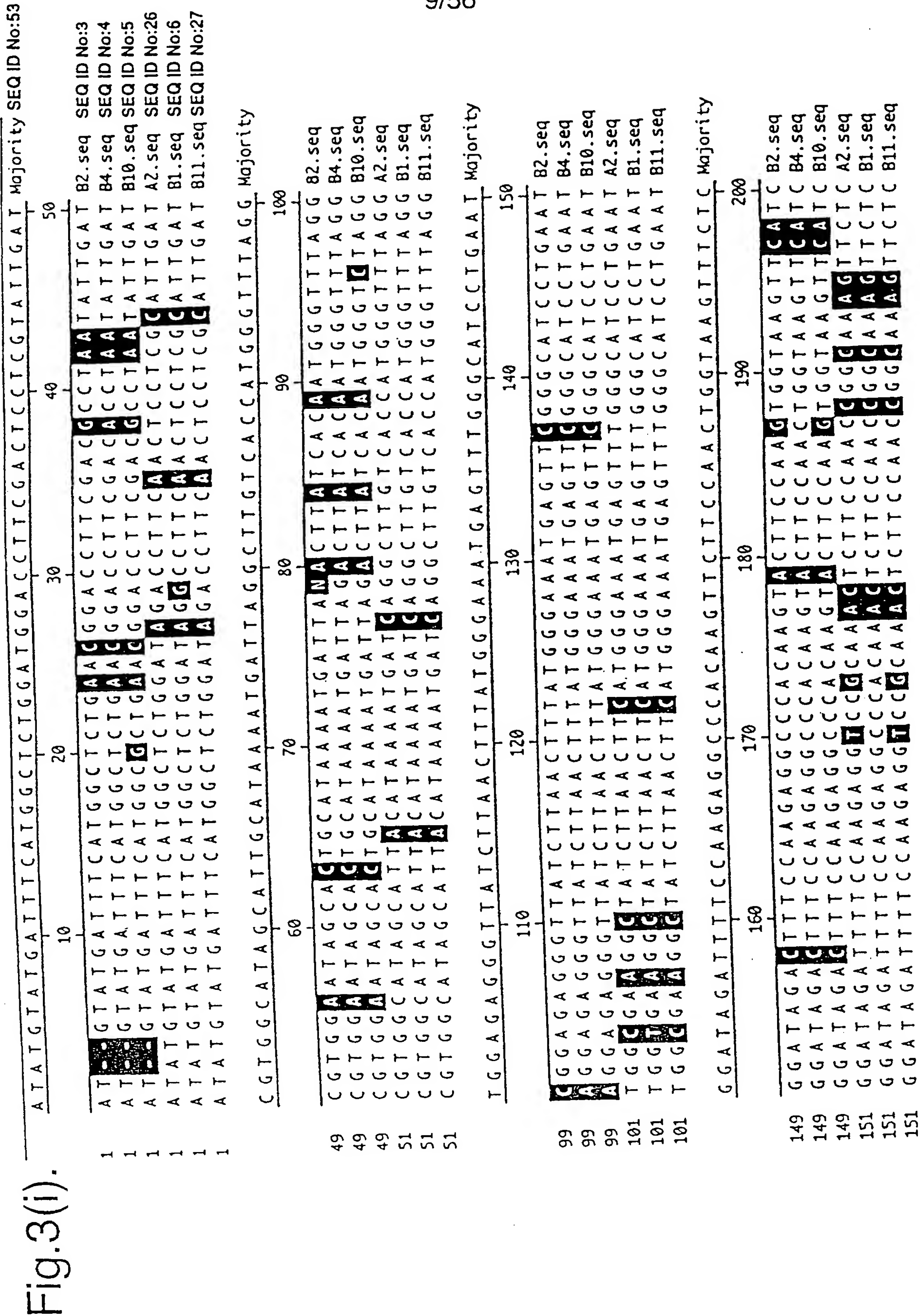


Fig.3(ii).

	C	C	T	G	G	A	A	T	A	C	A	A	T	A	G	T	T	A	T	G	A	T	A	A	T	G	C	C	G	T	C	G	T	A	G	A	T	T	T	G	A	T	C	T	T	G	G	Majority																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																						
	210	211	212	213	214	215	216	217	218	219	220	221	222	223	224	225	226	227	228	229	230	231	232	233	234	235	236	237	238	239	240	241	242	243	244	245	246	247	248	249	250	251	252	253	254	255	256	257	258	259	260	261	262	263	264	265	266	267	268	269	270	271	272	273	274	275	276	277	278	279	280	281	282	283	284	285	286	287	288	289	290	291	292	293	294	295	296	297	298	299	300	301	302	303	304	305	306	307	308	309	310	311	312	313	314	315	316	317	318	319	320	321	322	323	324	325	326	327	328	329	330	331	332	333	334	335	336	337	338	339	340	341	342	343	344	345	346	347	348	349	350	351	352	353	354	355	356	357	358	359	360	361	362	363	364	365	366	367	368	369	370	371	372	373	374	375	376	377	378	379	380	381	382	383	384	385	386	387	388	389	390	391	392	393	394	395	396	397	398	399	400	401	402	403	404	405	406	407	408	409	410	411	412	413	414	415	416	417	418	419	420	421	422	423	424	425	426	427	428	429	430	431	432	433	434	435	436	437	438	439	440	441	442	443	444	445	446	447	448	449	450	451	452	453	454	455	456	457	458	459	460	461	462	463	464	465	466	467	468	469	470	471	472	473	474	475	476	477	478	479	480	481	482	483	484	485	486	487	488	489	490	491	492	493	494	495	496	497	498	499	500	501	502	503	504	505	506	507	508	509	510	511	512	513	514	515	516	517	518	519	520	521	522	523	524	525	526	527	528	529	530	531	532	533	534	535	536	537	538	539	540	541	542	543	544	545	546	547	548	549	550	551	552	553	554	555	556	557	558	559	560	561	562	563	564	565	566	567	568	569	570	571	572	573	574	575	576	577	578	579	580	581	582	583	584	585	586	587	588	589	590	591	592	593	594	595	596	597	598	599	600	601	602	603	604	605	606	607	608	609	610	611	612	613	614	615	616	617	618	619	620	621	622	623	624	625	626	627	628	629	630	631	632	633	634	635	636	637	638	639	640	641	642	643	644	645	646	647	648	649	650	651	652	653	654	655	656	657	658	659	660	661	662	663	664	665	666	667	668	669	670	671	672	673	674	675	676	677	678	679	680	681	682	683	684	685	686	687	688	689	690	691	692	693	694	695	696	697	698	699	700	701	702	703	704	705	706	707	708	709	710	711	712	713	714	715	716	717	718	719	720	721	722	723	724	725	726	727	728	729	730	731	732	733	734	735	736	737	738	739	740	741	742	743	744	745	746	747	748	749	750	751	752	753	754	755	756	757	758	759	760	761	762	763	764	765	766	767	768	769	770	771	772	773	774	775	776	777	778	779	780	781	782	783	784	785	786	787	788	789	790	791	792	793	794	795	796	797	798	799	800	801	802	803	804	805	806	807	808	809	810	811	812	813	814	815	816	817	818	819	820	821	822	823	824	825	826	827	828	829	830	831	832	833	834	835	836	837	838	839	840	841	842	843	844	845	846	847	848	849	850	851	852	853	854	855	856	857	858	859	860	861	862	863	864	865	866	867	868	869	870	871	872	873	874	875	876	877	878	879	880	881	882	883	884	885	886	887	888	889	890	891	892	893	894	895	896	897	898	899	900	901	902	903	904	905	906	907	908	909	910	911	912	913	914	915	916	917	918	919	920	921	922	923	924	925	926	927	928	929	930	931	932	933	934	935	936	937	938	939	940	941	942	943	944	945	946	947	948	949	950	951	952	953	954	955	956	957	958	959	960	961	962	963	964	965	966	967	968	969	970	971	972	973	974	975	976	977	978	979	980	981	982	983	984	985	986	987	988	989	990	991	992	993	994	995	996	997	998	999	1000	1001	1002	1003	1004	1005	1006	1007	1008	1009	1010	1011	1012	1013	1014	1015	1016	1017	1018	1019	1020	1021	1022	1023	1024	1025	1026	1027	1028	1029	1030	1031	1032	1033	1034	1035	1036	1037	1038	1039	1040	1041	1042	1043	1044	1045	1046	1047	1048	1049	1050	1051	1052	1053	1054	1055	1056	1057	1058	1059	1060	1061	1062	1063	1064	1065	1066	1067	1068	1069	1070	1071	1072	1073	1074	1075	1076	1077	1078	1079	1080	1081	1082	1083	1084	1085	1086	1087	1088	1089	1090	1091	1092	1093	1094	1095	1096	1097	1098	1099	1100	1101	1102	1103	1104	1105	1106	1107	1108	1109	1110	1111	1112	1113	1114	1115	1116	1117	1118	1119	1120	1121	1122	1123	1124	1125	1126	1127	1128	1129	1130	1131	1132	1133	1134	1135	1136	1137	1138	1139	1140	1141	1142	1143	1144	1145	1146	1147	1148	1149	1150	1151	1152	1153	1154	1155	1156	1157	1158	1159	1160	1161	1162	1163	1164	1165	1166	1167	1168	1169	1170	1171	1172	1173	1174	1175	1176	1177	1178	1179	1180	1181	1182	1183	1184	1185	1186	1187	1188	1189	1190	1191	1192	1193	1194	1195	1196	1197	1198	1199	1200	1201	1202	1203	1204	1205	1206	1207	1208	1209	1210	1211	1212	1213	1214	1215	1216	1217	1218	1219	1220	1221	1222	1223	1224	1225	1226	1227	1228	1229	1230	1231	1232	1233	1234	1235	1236	1237	1238	1239	1240	1241	1242	1243	1244	1245	1246	1247	1248	1249	1250	1251	1252	1253	1254	1255	1256	1257	1258	1259	1260	1261	1262	1263	1264	1265	1266	1267	1268	1269	1270	1271	1272	1273	1274	1275	1276	1277	1278	1279	1280	1281	1282	1283	1284	1285	1286	1287	1288	1289	1290	1291	1292	1293	1294	1295	1296	1297	1298	1299	1300	1301	1302	1303	1304	1305	1306	1307	1308	1309	1310	1311	1312	1313	1314	1315	1316	1317	1318	1319	1320	1321	1322	1323	1324	1325	1326	1327	1328	1329	1330	1331	1332	1333	1334	1335	1336	1337	1338	1339	1340	1341	1342	1343	1344	1345	1346	1347	1348	1349	1350	1351	1352	1353	1354	1355	1356	1357	1358	1359	1360	1361	1362	1363	1364	1365	1366	1367	1368	1369	1370	1371	1372	1373	1374	1375	1376	1377	1378	1379	1380	1381	1382	1383	1384	1385	1386	1387	1388	1389	1390	1391	1392	1393	1394	1395	1396	1397	1398	1399	1400	1401	1402	1403	1404	1405	1406	1407	1408	1409	1410	1411	1412	1413	1414	1415	1416	1417	1418	1419	1420	1421	1422	1423	1424	1425	1426	1427	1428	1429	1430	1431	1432	1433	1434	1435	1436	1437	1438	1439	1440	1441	1442	1443	1444	1445	1446	1447	1448	1449	1450	1451	1452	1453	1454	1455	1456	1457	1458	1459	1460	1461	1462	1463	1464	1465	1466	1467	1468	1469	1470	1471	1472	1473	1474	1475	1476	1477	1478	1479	1480	1481	1482	1483	1484	1485	1486	1487	1488	1489	1490	1491	1492	1493	1494	1495	1496	1497	1498	1499	1500	1501	1502	1503	1504	1505	1506	1507	1508	1509	1510	1511	1512	1513	1514	1515	1516	1517	1518	1519	1520	1521	1522	1523	1524	1525	1526	1527	1528	1529	1530	1531	1532	1533	1534	1535	1536	1537	1538	1539	1540	1541	1542	1543	1544	1545	1546	1547	1548	1549	1550	1551	1552	1553	1554	1555	1556	1557	1558	1559	1560	1561	1562	1563	1564	1565	1566	1567	1568	1569	1570	1571	1572	1573	1574	1575	1576	1577	1578	1579	1580	1581	1582	1583	1584	1585	1586	1587	1588	1589	1590	1591	1592	1593	1594	1595	1596	1597	1598	1599	1600	1601	1602	1603	1604	1605	1606	1607	1608	1609	1610	1611	1612	1613	1614	1615	1616	1617	1618	1619	1620	1621	1622	1623

Fig. 3(iii).

[illegible]

Fig. 3(iv).

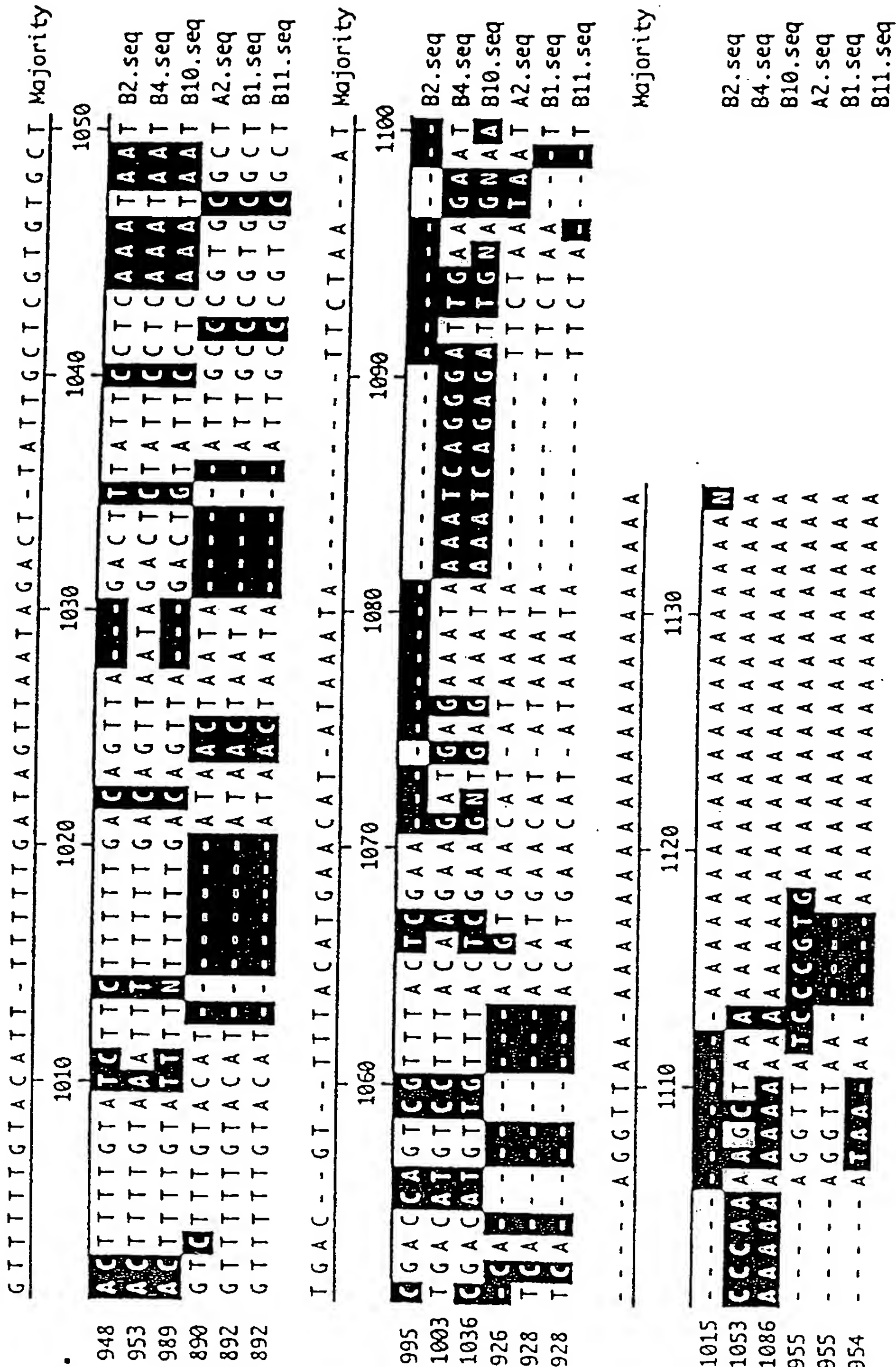
[illegible]

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Fig.3(v).

A T C G C C A T G G C G T T G G G A G G G G A T C G T G C T T C T T G T G T T A T - G C T T T G T Majority																																							
810 820 830 840 850																																							
794	T	C	C	C	C	A	G	G	C	G	T	T	G	T	G	A	A	A	A	C	A	T	G	C	T	C	A	T	T	T	A	T	B2.seq						
798	A	T	T	C	C	C	A	G	G	C	G	T	T	G	N	G	A	A	A	A	C	A	T	C	T	C	A	T	T	T	A	T	B4.seq						
793	T	C	C	C	C	A	G	G	N	G	T	T	G	T	G	A	A	A	A	C	A	T	C	A	T	C	A	T	T	T	A	T	B10.seq						
736	A	G	C	G	C	C	A	T	G	A	C	-	-	T	G	G	A	G	G	G	A	T	C	C	T	T	C	C	C	C	A	G	A	A2.seq					
736	A	G	C	G	C	C	A	T	G	A	C	-	-	T	G	G	A	G	G	G	A	T	C	C	T	T	C	C	C	C	A	G	A	B1.seq					
736	A	G	C	G	C	C	A	T	G	A	C	-	-	T	G	G	A	G	G	G	A	T	C	C	T	T	C	C	C	C	A	G	A	B11.seq					
G G A T C A G - G A T G G A A C - T C C C C T A G G T A G C C - - T T G T T G G T G A G C G C T C Majority																																							
860 870 880 890 900																																							
843	G	G	A	T	C	A	G	C	G	A	C	T	C	C	C	C	C	A	A	T	A	C	C	C	-	-	-	-	-	-	-	-	-	B2.seq					
848	G	G	A	T	C	A	G	N	G	A	A	C	C	T	C	C	C	C	A	A	T	A	C	C	-	-	-	-	-	-	-	-	-	B4.seq					
839	G	G	A	T	C	A	G	G	A	N	G	A	A	C	C	T	C	C	C	A	A	N	A	C	C	C	T	T	T	T	T	T	T	T	B10.seq				
783	G	G	A	G	C	A	G	-	-	A	T	G	G	A	-	-	-	-	T	A	G	G	T	A	G	C	-	-	-	-	-	-	-	-	A2.seq				
783	G	G	A	G	C	A	G	-	-	A	T	G	G	A	-	-	-	-	T	A	G	G	T	A	G	C	-	-	-	-	-	-	-	-	B1.seq				
783	G	G	A	T	C	A	G	-	-	A	T	G	G	A	-	-	-	-	T	A	G	G	T	A	G	C	-	-	-	-	-	-	-	-	B11.seq				
G A A G A A - - - A A T G G A C G G G C C T G G G T G T T T G C T T A A A - T T T T G T T G C C Majority																																							
910 920 930 940 950																																							
874	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	B2.seq					
879	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	B4.seq					
889	G	A	T	A	G	G	C	C	C	G	G	T	N	T	C	T	G	C	A	T	N	T	G	G	A	T	T	T	T	T	T	T	T	T	B10.seq				
819	G	A	A	G	A	A	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	A2.seq				
819	G	A	A	G	A	A	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	B1.seq				
819	G	A	A	G	A	A	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	B11.seq				
C T A A A C C C T C G C T C C T A T C T T G T A C A T T G C C G G T T T A G - A T A G - G G T T - T Majority																																							
960 970 980 990 1000																																							
898	G	T	A	A	A	C	C	A	T	T	G	C	T	A	G	T	G	T	C	T	A	A	T	T	G	A	C	A	T	A	G	A	G	G	T	T	B2.seq		
903	C	T	A	A	A	C	C	A	T	T	G	C	T	A	A	C	T	A	T	C	C	A	A	T	T	G	A	C	A	T	A	G	A	G	G	T	T	B4.seq	
939	A	T	A	A	A	C	C	A	T	T	G	C	T	A	G	T	G	T	C	C	T	N	T	A	A	T	T	A	G	A	T	A	G	A	G	G	T	T	B10.seq
858	C	T	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	A2.seq		
858	C	T	G	A	A	C	C	C	T	C	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	B1.seq		
858	C	T	T	A	A	C	C	C	T	C	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	B11.seq		

Fig.3(vi).



Decoration 'Decoration #1': Shade (with solid black) residues that differ from the Consensus.

Fig.3A.

		Percent Similarity							
Percent Divergence		1	2	3	4	5	6		
	1		91.0	94.4	59.0	60.0	59.5	1	B2.seq
	2	4.5		89.2	58.8	59.9	59.6	2	B4.seq
	3	2.4	4.6		59.3	59.6	59.8	3	B10.seq
	4	32.6	32.3	34.3		95.5	95.7	4	A2.seq
	5	30.5	29.7	32.0	2.1		96.8	5	B1.seq
	6	31.6	30.9	32.6	2.4	2.7		6	B11.seq
		1	2	3	4	5	6		

Fig.4A.

		Percent Similarity					
Percent Divergence		1	2	3	4		
	1		88.7	81.7	85.0	1	Maizellb.pro
	2	10.8		82.2	82.6	2	B6.pro
	3	17.9	17.5		86.9	3	B11.pro
	4	14.6	17.0	12.7		4	Maizella.pro
		1	2	3	4		

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Fig.4.

1	M	Y	D	F	M	A	L	D	R	P	S	T	P	T	I	D	R	G	I	A	L	H	K	M	I	R	L	I	T	M	MaizeIIb.pro	SEQ ID No: 30
1	M	Y	D	F	M	A	L	N	G	P	S	T	P	N	I	D	R	G	I	A	L	H	K	M	I	R	L	I	T	M	B6.pro	SEQ ID No: 7
1	M	Y	D	F	M	A	L	D	R	P	S	T	P	R	I	D	R	G	I	A	L	H	K	M	I	R	L	V	T	M	B11.pro	SEQ ID No: 28
1	M	Y	D	F	M	A	L	D	R	P	S	T	P	R	I	D	R	G	I	A	L	H	K	M	I	R	L	V	T	M	MaizeIIa.pro	SEQ ID No: 29
31	G	L	G	G	E	G	Y	L	N	F	M	G	N	E	F	G	H	P	E	W	I	D	F	P	R	G	P	Q	R	L	MaizeIIb.pro	
31	G	L	G	G	E	G	Y	L	N	F	M	G	N	E	F	G	H	P	E	W	I	D	F	P	R	G	P	Q	V	L	B6.pro	
31	G	L	G	G	E	G	Y	L	N	F	M	G	N	E	F	G	H	P	E	W	I	D	F	P	R	G	P	Q	T	L	B11.pro	
31	G	L	G	G	E	G	Y	L	N	F	M	G	N	E	F	G	H	P	E	W	I	D	F	P	R	G	P	Q	S	L	MaizeIIa.pro	
61	P	S	G	K	F	I	P	G	N	N	S	Y	D	K	C	R	R	R	F	D	L	G	D	A	D	Y	L	R	Y	MaizeIIb.pro		
61	P	S	G	K	F	I	P	G	N	S	N	S	Y	D	K	C	R	R	R	F	D	L	G	D	A	E	F	L	R	Y	B6.pro	
61	P	T	G	K	V	L	P	G	N	N	S	Y	D	K	C	R	R	R	F	D	L	G	D	A	D	F	L	R	Y	B11.pro		
61	P	N	G	S	V	I	P	G	N	N	S	F	D	K	C	R	R	R	F	D	L	G	D	A	D	Y	L	R	Y	MaizeIIa.pro		
91	H	G	M	Q	E	F	D	Q	A	M	Q	H	L	E	Q	K	Y	E	F	M	T	S	D	H	Q	Y	I	S	R	K	MaizeIIb.pro	
91	H	G	M	Q	O	F	D	Q	A	M	Q	H	L	E	E	K	Y	G	F	M	T	S	D	H	Q	Y	V	S	R	K	B6.pro	
91	R	G	M	Q	E	F	D	Q	A	M	Q	H	L	E	E	K	Y	G	F	M	T	S	E	H	Q	Y	V	S	R	K	B11.pro	
91	R	G	M	Q	E	F	D	Q	A	M	Q	H	L	E	G	K	Y	E	F	M	T	S	D	H	S	Y	F	S	R	K	MaizeIIa.pro	
121	H	E	E	D	K	V	I	V	F	E	K	G	D	L	V	F	V	F	N	F	H	C	N	N	S	Y	F	D	Y	R	MaizeIIb.pro	
121	H	E	E	D	K	V	I	V	F	E	K	G	D	L	V	F	V	F	N	F	H	W	S	N	S	Y	F	D	Y	R	B6.pro	
121	H	E	E	D	K	V	I	I	F	E	R	G	D	L	V	F	V	F	N	F	H	W	S	N	S	F	F	D	Y	R	B11.pro	
121	H	E	E	D	K	V	I	I	F	E	R	G	D	L	V	F	V	F	N	F	H	W	S	N	S	Y	F	D	Y	R	MaizeIIa.pro	
151	I	G	C	R	K	P	G	V	Y	K	V	V	L	D	S	D	A	G	L	F	G	G	F	S	R	I	H	H	A	A	MaizeIIb.pro	
151	V	G	C	L	K	P	G	K	Y	K	V	V	L	D	S	D	A	G	L	F	G	G	F	G	R	I	H	H	T	A	B6.pro	
151	V	G	C	S	K	P	G	K	Y	K	V	A	L	D	S	D	D	A	L	F	G	G	F	S	R	L	D	H	E	V	B11.pro	
151	V	G	C	F	K	P	G	K	Y	K	I	V	L	D	S	D	D	G	L	F	G	G	F	S	R	L	D	H	E	A	MaizeIIa.pro	
181	E	H	F	T	A	D	C	S	H	D	N	R	P	Y	S	F	S	V	Y	T	P	S	R	T	C	V	V	Y	A	P	MaizeIIb.pro	
181	E	H	F	T	S	D	C	Q	H	D	N	R	P	H	S	F	S	V	Y	T	P	S	R	T	C	V	V	Y	A	P	B6.pro	
181	D	V	F	T	T	E	H	P	H	D	N	R	P	R	S	F	L	V	Y	T	P	S	R	T	A	V	V	Y	A	L	B11.pro	
181	E	Y	F	T	A	D	W	P	H	D	N	R	P	C	S	F	S	V	Y	A	P	S	R	T	A	V	V	Y	A	P	MaizeIIa.pro	
211	V	-	-	-	E	MaizeIIb.pro		
211	M	-	-	-	N	B6.pro		
211	T	-	-	-	E	B11.pro		
211	A	G	A	E	D	E	MaizeIIa.pro		

Decoration 'Decoration #1': Shade (with solid black) residues that differ from MaizeIIb.pro.

Fig.5.

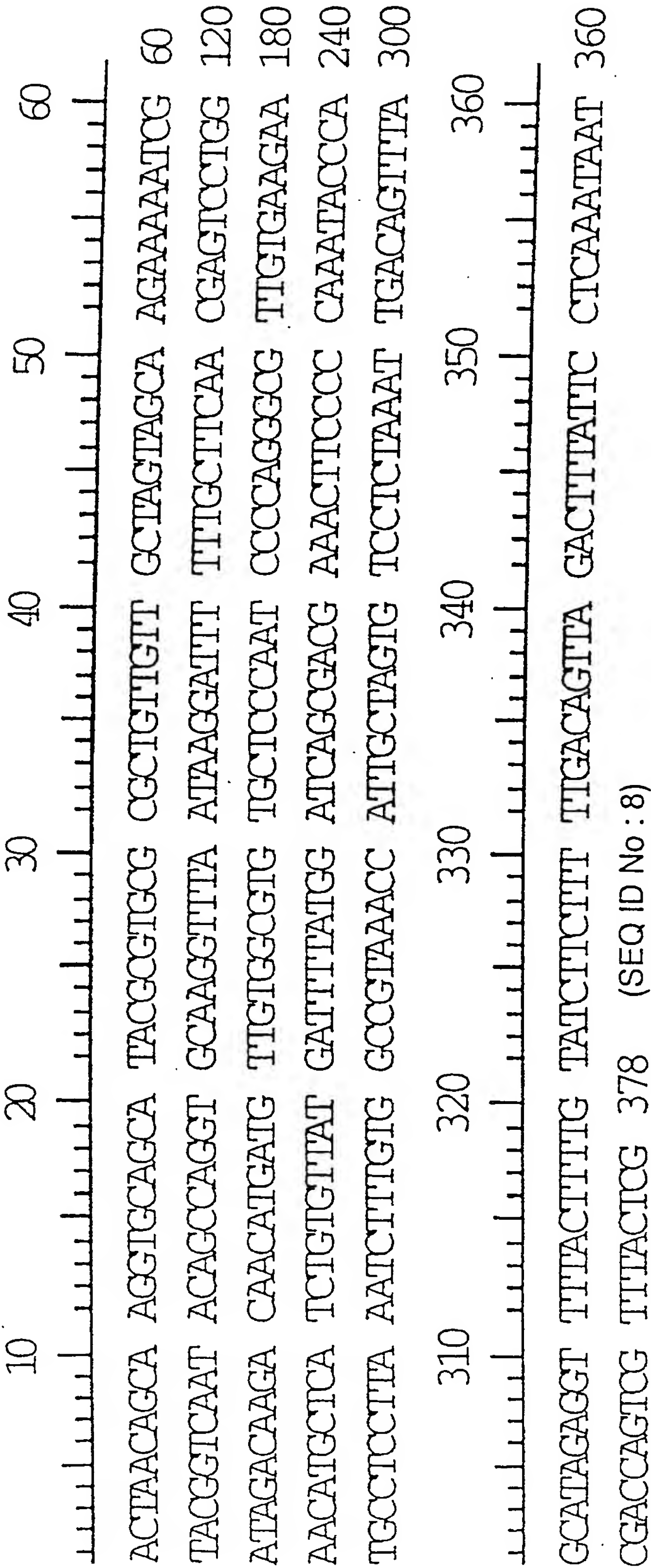


Fig.6.

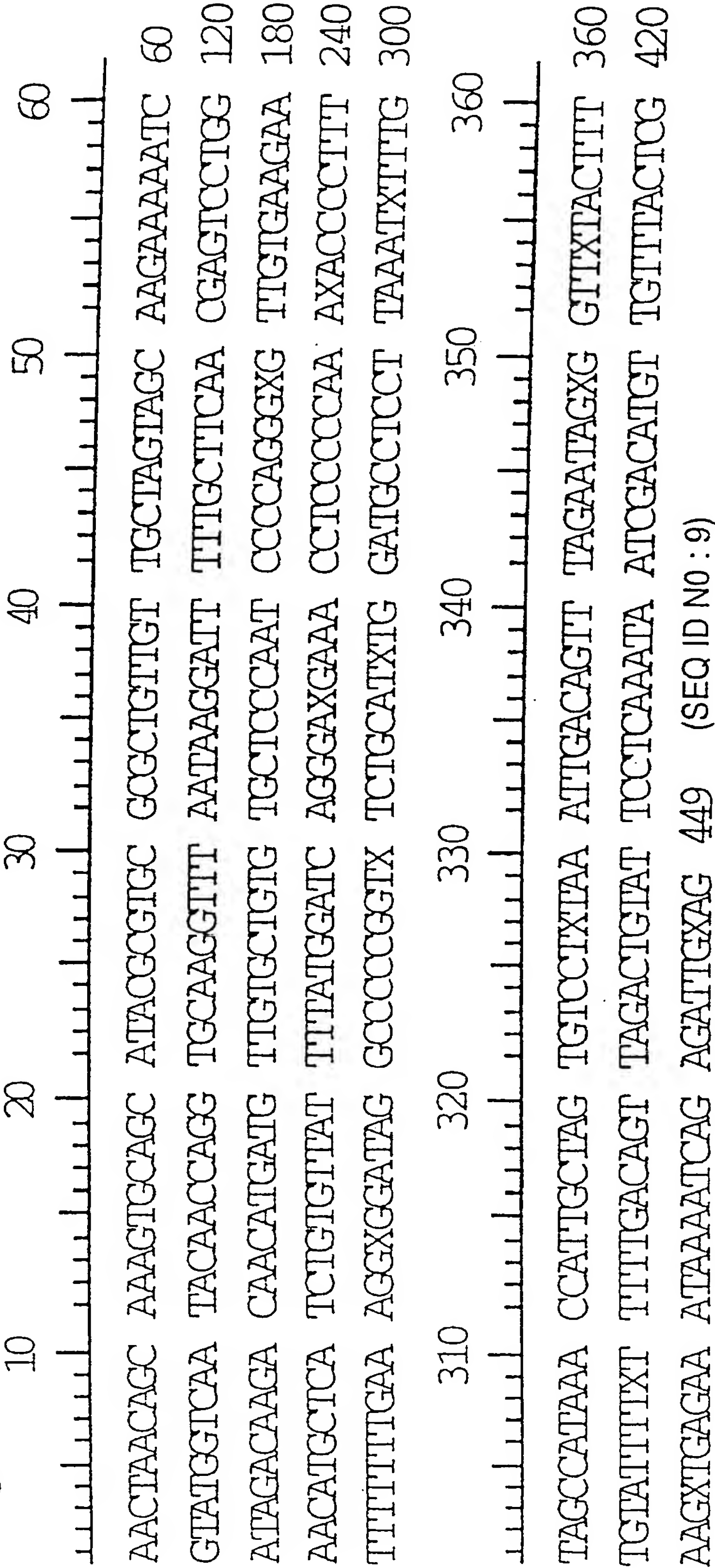


Fig.7.

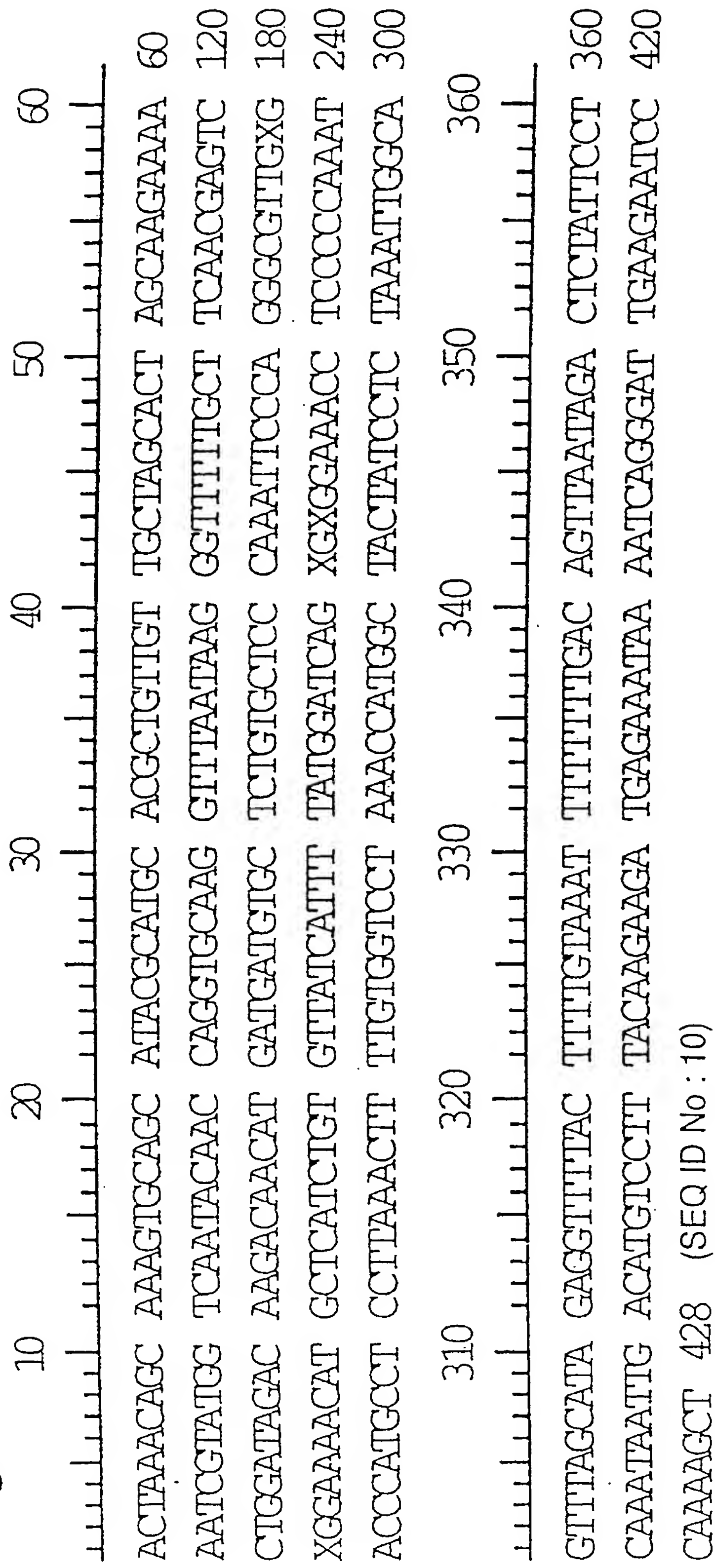


Fig.8(i).

1	A	A	C	T	A	A	C	A	G	C	A	A	G	T	G	C	A	G	C	A	T	A	C	G	C	G	T	G	C	B10-3'.seq	
1	A	-	C	T	A	A	C	A	G	C	A	A	G	T	G	C	A	G	C	A	T	A	C	G	C	G	T	G	C	B2-3'.seq	
1	A	C	T	A	A	C	A	G	C	A	A	G	T	G	C	A	G	C	A	T	A	C	G	C	A	T	G	C	B4-3'.seq		
1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	ZMSBE2b-3'.seq		
31	G	C	G	C	T	G	T	T	G	C	T	A	G	-	-	-	T	A	G	C	A	A	G	A	A	A	A	A	A	B10-3'.seq	
30	G	C	G	C	T	G	T	T	G	C	T	A	G	-	-	-	T	A	G	C	A	A	G	A	A	A	A	A	A	B2-3'.seq	
31	A	C	G	C	T	G	T	T	G	C	T	A	G	C	A	C	T	A	G	C	A	A	G	A	A	A	A	A	A	B4-3'.seq	
12	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	ZMSBE2b-3'.seq		
58	A	-	T	C	G	T	A	T	G	G	T	C	A	A	T	A	C	A	C	A	G	G	T	G	C	A	A	G	B10-3'.seq		
57	A	-	T	C	G	T	A	C	G	T	C	A	A	T	A	C	A	G	C	A	G	G	T	G	C	A	A	G	B2-3'.seq		
61	A	A	T	C	G	T	A	T	G	G	T	C	A	A	T	A	C	A	C	A	G	G	T	G	C	A	A	G	B4-3'.seq		
28	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	ZMSBE2b-3'.seq		
87	G	T	T	A	A	T	A	A	G	G	A	T	T	T	T	T	T	-	G	C	T	T	C	A	A	C	G	A	G	T	B10-3'.seq
86	G	T	T	A	A	T	A	A	G	G	A	T	T	T	T	T	T	T	G	C	T	T	C	A	A	C	G	A	G	T	B2-3'.seq
91	G	T	T	A	A	T	A	A	G	G	A	T	T	T	T	T	T	-	G	C	T	T	C	A	A	C	G	A	G	T	B4-3'.seq
50	G	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	ZMSBE2b-3'.seq	
116	C	C	T	G	G	A	T	A	G	A	C	A	A	G	A	C	A	A	C	A	T	G	A	T	G	T	G	T	G	B10-3'.seq	
116	C	C	T	G	G	A	T	A	G	A	C	A	A	G	A	C	A	A	C	A	T	G	A	T	G	T	G	T	G	B2-3'.seq	
120	C	C	T	G	G	A	T	A	G	A	C	A	A	G	A	C	A	A	C	A	T	G	A	T	G	T	G	T	G	B4-3'.seq	
70	C	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	ZMSBE2b-3'.seq	
146	C	T	G	T	G	T	G	C	T	C	C	A	A	-	T	C	C	C	C	A	G	G	G	N	G	T	G	T	G	T	B10-3'.seq
146	G	C	G	T	G	T	G	C	T	C	C	A	A	-	T	C	C	C	C	A	G	G	G	C	G	T	T	G	T	B2-3'.seq	
150	C	T	C	T	G	T	G	C	T	C	C	A	A	A	T	T	C	C	C	A	G	G	G	C	G	T	T	G	N	B4-3'.seq	
87	C	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	ZMSBE2b-3'.seq	
175	G	A	A	G	A	A	A	C	A	T	G	C	T	C	A	T	C	T	G	T	G	T	A	T	-	-	-	-	-	-	B10-3'.seq
175	G	A	A	G	A	A	A	C	A	T	G	C	T	C	A	T	C	T	G	T	G	T	A	T	G	A	T	T	T	B2-3'.seq	
180	G	N	G	G	A	A	A	C	A	T	G	C	T	C	A	T	C	T	G	T	G	T	A	T	C	A	T	T	T	B4-3'.seq	
103	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	ZMSBE2b-3'.seq	
202	T	T	A	T	G	G	A	T	C	A	G	G	G	A	N	G	A	A	C	C	T	C	C	C	C	C	C	A	A	A	B10-3'.seq
205	T	T	A	T	G	G	A	T	C	A	G	C	G	A	C	C	A	A	C	T	T	C	C	C	C	C	C	A	A	A	B2-3'.seq
210	T	T	A	T	G	G	A	T	C	A	G	N	G	N	G	A	A	A	C	C	T	C	C	C	C	C	C	A	A	A	B4-3'.seq
112	T	T	A	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	ZMSBE2b-3'.seq

Fig. 8(ii)

232	N	A	C	C	C	C	T	T	T	T	T	T	T	T	T	T	G	A	A	A	G	G	N	G	G	A	T	A	G	B10-3'.seq		
235	T	A	C	C	C	C	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	B2-3'.seq	
240	T	A	C	C	C	C	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	B4-3'.seq	
120	T	G	C	-	-	-	-	-	-	-	-	-	-	-	-	-	T	G	G	A	A	A	G	C	C	C	A	T	G	C	A	ZMSBE2b-3'.seq
262	C	C	C	C	G	G	T	N	T	C	T	G	C	A	T	N	T	G	G	A	T	G	C	C	C	T	C	C	T	C	T	B10-3'.seq
240	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	A	T	G	C	C	T	C	C	T	T	T	B2-3'.seq	
245	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	A	T	G	C	C	T	C	C	T	T	T	B4-3'.seq	
138	T	C	-	-	-	-	-	T	C	G	C	T	G	C	G	T	T	-	-	G	T	-	C	C	T	C	T	C	T	C	T	ZMSBE2b-3'.seq
292	A	A	A	T	N	T	T	T	G	T	A	G	C	C	A	T	A	A	A	C	C	A	T	T	G	C	T	A	G	T	B10-3'.seq	
250	A	A	A	T	C	T	T	T	G	T	G	G	C	C	G	T	A	A	A	C	C	A	T	T	G	C	T	A	G	T	B2-3'.seq	
255	A	A	A	C	T	T	T	T	G	T	G	G	T	C	C	T	A	A	A	C	C	A	T	G	G	C	T	A	C	T	B4-3'.seq	
159	A	-	-	-	-	-	-	-	T	A	-	-	-	-	T	A	T	A	A	-	-	-	-	-	-	-	-	-	-	-	-	ZMSBE2b-3'.seq
322	G	T	C	C	C	T	N	T	A	A	A	T	T	G	A	C	A	G	T	T	A	G	A	A	T	A	G	N	G	G	B10-3'.seq	
280	G	T	C	C	C	T	C	T	A	A	A	T	T	G	A	C	A	G	T	T	A	G	C	A	T	A	G	A	G	G	B2-3'.seq	
285	A	T	C	C	C	T	C	T	A	A	A	T	T	G	A	C	A	G	T	T	A	G	C	A	T	A	G	A	G	G	B4-3'.seq	
169	G	A	C	C	C	T	T	C	A	A	G	G	T	G	T	C	A	A	T	T	A	A	C	A	T	A	G	A	G	T	ZMSBE2b-3'.seq	
352	T	T	N	T	A	C	T	T	T	T	T	G	T	A	T	T	T	T	T	T	T	T	T	T	G	A	C	A	G	T	B10-3'.seq	
310	T	T	T	A	C	T	T	T	T	T	T	G	T	A	T	C	T	T	T	T	T	T	T	T	G	A	C	A	G	T	B2-3'.seq	
315	T	T	T	A	C	T	T	T	T	T	T	G	T	A	A	A	T	T	T	T	T	T	T	T	G	A	C	A	G	T	B4-3'.seq	
199	T	T	T	C	G	T	T	T	T	T	T	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	ZMSBE2b-3'.seq
382	A	-	-	-	G	A	C	T	G	T	A	T	T	C	C	T	C	A	A	T	A	A	T	C	G	A	C	A	T	B10-3'.seq		
340	A	-	-	-	G	A	C	T	T	A	T	T	C	C	T	C	A	A	T	A	A	T	C	G	A	C	C	A	C	A	B2-3'.seq	
345	A	A	T	A	G	A	C	T	C	T	A	T	T	C	C	T	C	A	A	T	A	A	T	T	G	A	C	A	T	B4-3'.seq		
209	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	ZMSBE2b-3'.seq

Fig.8(iii).

409	G	T	G	T	T	A	C	T	C	G	A	A	G	N	T	G	A	A	T	A	A	T	C	B10-3'.seq
367	G	T	C	G	T	T	A	C	T	C	G													B2-3'.seq
375	G	T	C	C	T	T	A	C	A	A	G	A	T	G	A	G	A	A	T	A	A	T	C	B4-3'.seq
209	-	-	C	G	C	T	T	C	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	ZMSBE2b-3'.seq
439	A	G	A	G	A	T	T	G	N	A	G													B10-3'.seq
378																								B2-3'.seq
405	A	G	G	A	T	T	G	A	A	G	A	T	C	C	C	A	A	A	G	C	T			B4-3'.seq
216	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	ZMSBE2b-3'.seq

Decoration 'Decoration #1': Shade (with solid black) residues that differ from B10-3'.seq.

Fig.8A.

Percent Similarity					Percent Divergence				
	1	2	3	4		1	2	3	4
1		88.9	76.2	26.3	1				
2	4.1		81.2	31.8	2				
3	7.2	9.4		29.5	3				
4	33.5	32.6	33.9		4				
	1	2	3	4					

B10-3'.seq
B2-3'.seq
B4-3'.seq
ZMSBE2b-3'.seq

Fig.9A.

Chinese Spring

N2AT2B

N2BT2D

N2DT2A

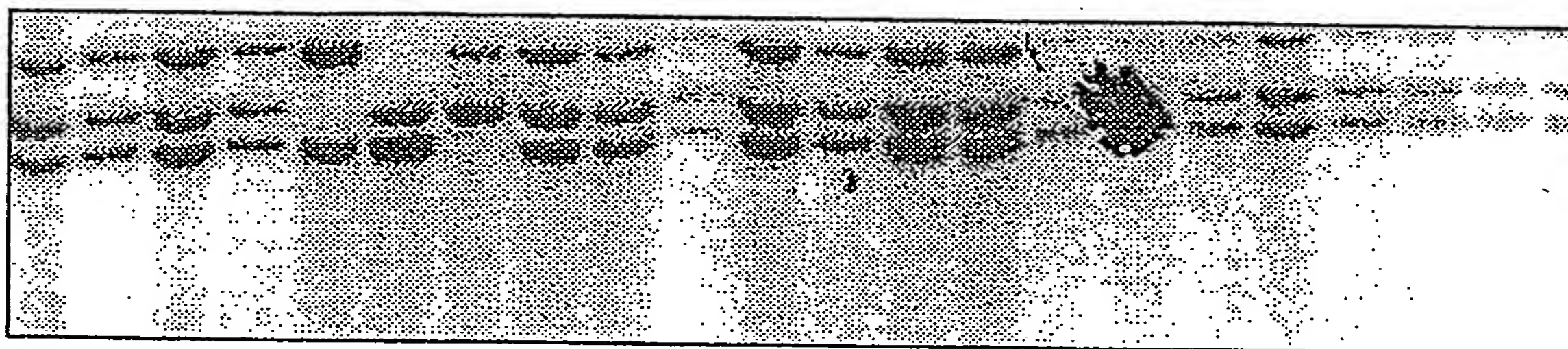


Fig.9B.

Chinese Spring

N2AT2B
N2BT2D
N2DT2A

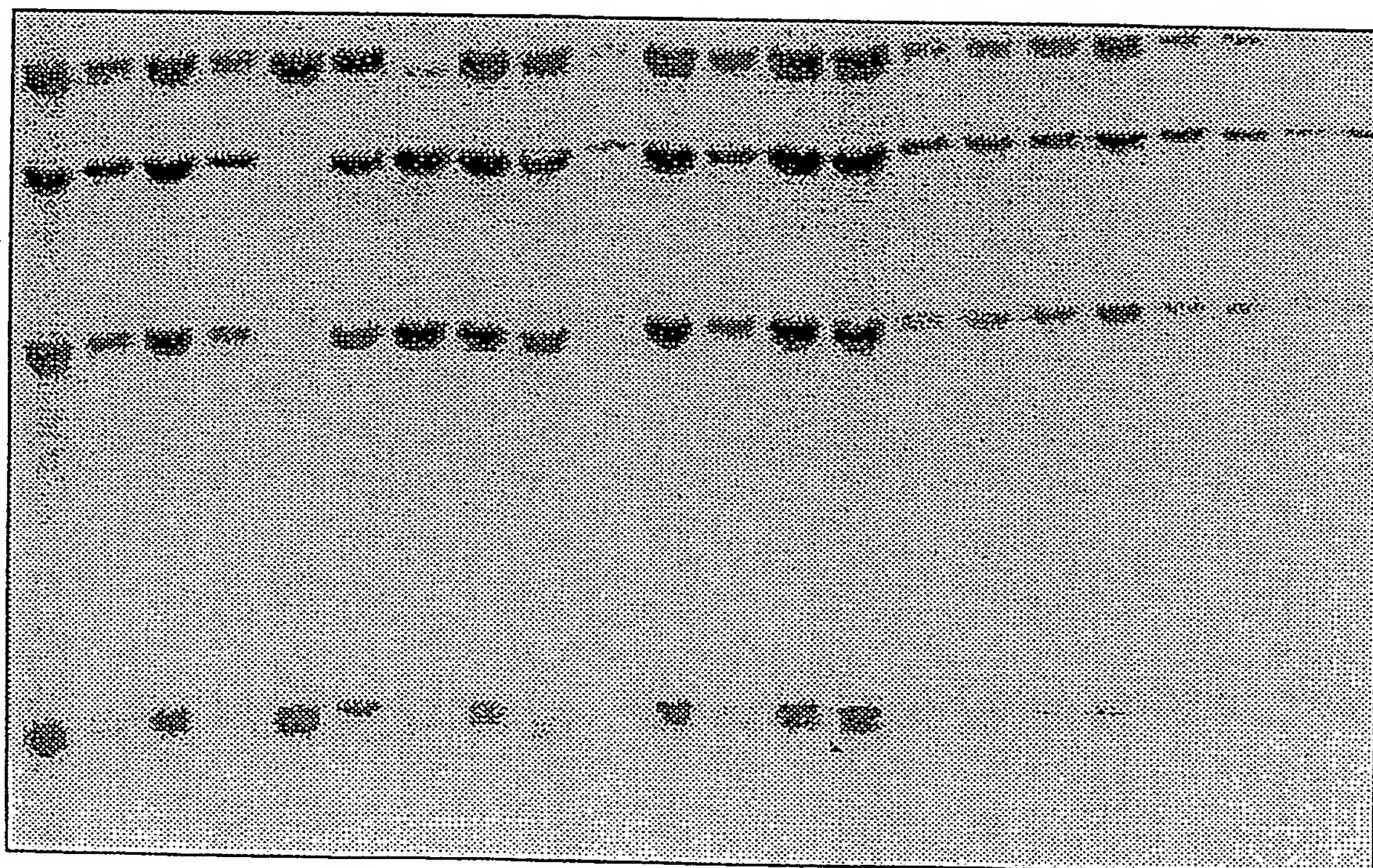


Fig.10(i).

CATYGACGGCCAGTGACITCGAGCTCGGTACCCGGGATCCGATTGGTGTGTGGAGATGTTCTTGCCAAACAATGCAGATGGTTCCGCC 90 SEQ ID No:1
I D G O . L R A R Y P G I R F G V W E M F L P N N A D G S P SEQ ID No:2
ACCAATTCCITCACGGCTCACGGGTGAAGGTGAGAAATGGATACTCCATCTGGGATAAAGGATTCAATTCCTGCTIGGATCAAGTACTCCGT 180
P I P H G S R V K V R M D T P S G I K D S I P A W I K Y S V
GCAGACTCCAGGAGATATACCATACAATGGAATATATTATGATCCTCCGAAGAGGAGAAGTATGTATTCAAGCATCCTCAACCTAAACG 270
Q T P G D I P Y N G I Y Y D P P E E E K Y V F K H P Q P K R
ACCAAAATCATTTGCGGATATATGAACACATGTITGGCATGAGTAGCCCGGAACCAAGATCAACACATATGCCAAACTTCAGGGATGAGGT 360
P X S L R I Y E T H V G M S S P E P K I N T Y A N F R D E V
GCTTCCAAGAAATTAAAGACTTGGGATACAAATGCAGTGCAATAATGGCAATCCAGGACCTCATACTATGGAAGCTTTGGGTACCAITGT 450
L P R I K R L G Y N A V Q I M A I Q E H S Y Y G S F G Y H V
TACCAATTTCTTTGCACCAAGTAGCCGTTTGGGTCCCCAGAAAGATTTAAATCTTTGATTGATAGAGCTCAGGAGCTTGGCTTGGTGTGT 540
T N F F A P S S R F G S P E D L K S L I D R A H E L G L V V
CCTCATGGATGTTGTTACAGTCACGCGTCAAAATAATACCTTGGACGGGTGGAATGGTTTGGATGGCAGGATACACATTACTTCCATGG 630
L M D V V H S H A S N N T L D G L N G F D G T D T H Y F H G
CGGTTACGGGGCCATCAGTGGATGTGGGATTCCCGTGTGTTAACTATGGGAATAAGGAAGTTATAAGGTTTCTACTTTCCAATGCAAG 720
G S R G H H W M W D S R V F N Y G N K E V I R F L L S N A R
ATGGTGGCTAGAGGAGTATAAGTTTGATGTTTCCGATTGCGTGGCGGACCTCCATGATGTATACCCATCATGATTACAAGTAACCTT 810
W W L E E Y K F D G F R F D G A T S M M Y T H H G L Q V T F

Fig. 10(ii).

TACAGGAAGCTACCATGAATAATTTGGCTTTGCCACTGATGTAGATCGCGTCGTTTACTTGATGCTGATGAATGATCTAATTCATGGGTT 900
 T G S Y H E Y F G F A T D V D A V V Y L M L M N D L I H G F
 TTATCCTGAAGCCGTAACCTATCGGTGAAGATGTTAGTGAATGCCTACATTGGCCCTTCCTGTTCAAGTTGGTGGGTTGGTTTGACTA 990
 Y P E A V T I G E D V S G M P T F A L P V Q V G G V G F D Y
 TCGCTTACATATGGCTGTTGCCGACAAATGGATTGAACCTTCTCAAGGAACGATGAAGCTTGGGAGATGGGTAATATTGTGCACACACT 1080
 R L H M A V A D K W I E L L K G N D E A W E M G N I V H T L
 AACAAACAGAAGGTGGCCGAAAGTGTTACTTATGCTGAAAGTCACGATCAAGCACTGGTTGGAGACAAGACTATTGCATICTGGTT 1170
 T N R R W P E K C V T Y A E S H D Q A L V G D K T I A F W L
 GATGGACAAGGATAIGTATGATTTCATGGCTCIGAACGGACCTTCGACACCTAGTATTGATCGTGGAAATAGCACTGCATAAAATGATTAG 1260
 M D K D M Y D F M A L N G P S T P S I D R G I A L H K M I R
 ACTTATCACAATGGGTTTAGGAGGAGAGGGTTATCTTAACCTTTATGGGAAATGAGTTCGGGCATCCTGAATGGATAGACTTICCAAGAGG 1350
 L I T M G L G G E G Y L N F M G N E F G H P E W I D F P R G
 CCCACAAGTACTTCCAACCTGGTAAGTTTCATCCCGAGGAACAACAACAGTTACGACAAATGCCGTCGAAGATTGACCAGGGTGATGCAGA 1440
 P Q V L P T G K F I P G N N S Y D K C R R R F D Q G D A E
 ATTTCTTAGGTATCATGGTATGCAGCAGTTTGATCAGCGGATGCAGCATCTTGAGGAAAAATATGGCTTTATGACATCAGACCACCAGTA 1530
 F L R Y H G M Q Q F D Q A M Q H L E E K Y G F M T S D H Q Y
 CGTATCTCGGAAACATGAGGAAGATAAGGTGATCGTGTGTTGAAAAAGGGGACTTGGTATTGTGTTCAACTTCCACTGGAGTAATAGCTA 1620
 V S R K H E E D K V I V F E K G D L V F V F N F H W S N S Y

26/56

TTTTCGACTACCGGTTGGCTGTTTAAAGCCTGGGAAGTACAAGGTTGCTTTAGACTCAGACCGGACTCTTTGGTGGAATTGGTAGGAT 1710

F D Y R Y G C L K P G K Y K V V L D S D A G L F G G F G R I

CCCATCACACTGCAGAGCACTTCACTTCTGACTGCCAACATGACAACAGGCCCAATTGGTTCTCAGTGTA CACTCCTAGCAGAACCTGTGT 1800

HHHTAEHFTTSDDCQH DNRPHSHSVYTPSPSRTCV

GTGCTATGCTCCAATGAACAAAGTGCAGCATACGCATGCACGCTGTTGCTAGCACTAGCAAGAAAAATCGTATGGTCA 1890

V Y A P M N . T A K C S I R M H A V V A S T S K K K S Y C G Q

ATACAACCGTGCAAGGTTTAATAAGGTTTGCTTCAACGAGTCTGGATAGACAAGACAACATGATGATGCTCTGTGCTCCCAAAT 1980

Y N Q V Q G L I R V C F N E S W I D K T T . . C A L C S Q I

TCACCAGGCGTTGTGGAGAAAAATGCTCATCTGTGTTATTTATGGATCAGGGANGAAACCTCCCCCAAANACCCCTTTTTTTTGAA 2070

P R A L W R K N A H L C Y F M D Q G ? N L P Q ? P L F F L K

AGGNGGATAGGCCCCCGGINTCTGCAINTGGATGCCCTCCTAAATTTGTAGCCATAAACCAATTGCTAGTGCTCTNTAAATTGACAGTT 2160

G G . A P G ? C ? W M P P . ? F V A I N H C . C P ? N . Q F

TAGAAATAGNGGTTNTACTTTTGTATTTTNTTTTGTACAGTTAGACTGTATTCCTCAAAATAATCGACATGTTGTTTACTCGAAGNTGAGAA 2250

R I ? V ? L L Y F ? F D S . T V F L K . S T C C L L E ? E K

[illegible]

N Q R L ? ? K K K K K K K K K K K K K K K K

Fig. 11(i).

	10	20	30	40	50	Majority
52	M L C L	S S S L L P R P			S A	TASBE102 SEQ ID No:32
116	M L C L	A P S C S P L P R P			S R P	TASBEI SEQ ID No:33
44						0sbeII-1ALL SEQ ID No:11
151	M A T F A V S G W T L G V A R P A G A G G L L P R S G S E R R G G V D L P S L L R K K D S S R A					Wheat SBEII-2 SEQ ID No:34
	A A D R P X - P G I - - X G G G X X R L S A V P A - P X X L R - - - W X W P R K					Majority
94	A A D R P L - P G I I A G G G G K R L S V P S V P F L L R - - - W L W P R K					TASBE102
76	A A D R P G - P G I - - S G G G N V R L S A V P A - P S S L R - - - W S W P R K					TASBEI
44						0sbeII-1ALL
301	V L S R A A S P G K V L V P D G E S D D L A S P A Q P E E L Q I P E D I E E Q T A E V N M T G G T A					Wheat SBEII-2
	A K S K S S V P V X A X X X I X A T X X G V X X L P - - - I Y D L D P					Majority
202	A K S K S F V S V T A R G N K I A A T T G Y G S D H L P - - - I Y D L D L					TASBE102
175	A K S K F S V P V S A P R D Y T M A T A E D G V G D L P - - - I Y D L D P					TASBEI
44						0sbeII-1ALL
451	E K L E S S E P T Q G I V E T I T D G V T K G V K E L V V G E K P R V V P K P G D G Q K I Y E I D P					Wheat SBEII-2
	K L A X F K X H F D Y R X X X Y X X Q K H X I E K H E G G L E E F S K G Y L K F G I N T E X X A X V					Majority
304	K L A E F K D H F D Y T R N R Y I E Q K H L I E K H E G S L E E F S K G Y L K F G I N T E H G A S V					TASBE102
277	K F A G F K E H F S Y R M K K Y L D Q K H S I E K H E G G L E E F S K G Y L K F G I N T E N D A T V					TASBEI
44						0sbeII-1ALL
601	T I K D E R S H L D Y R Y S E Y R R I R A A I D Q H E G G L E A F S R G Y E K L G F T R S A E G I T					Wheat SBEII-2
	Y R E W A P A A X X A Q L V G D F N N W N G S G H X M T K D N F G V W S I R L S N N A D G S P A I P					Majority
454	Y R E W A P A A E E A Q L V G D F N N W N G S G H K M A K D N F G V W S I R I S H - V N G K P A I P					TASBE102
427	Y R E W A P A A M D A Q L I G D F N N W N G S G H R M T K D N Y G V W S I R I S H - V N G K P A I P					TASBEI
44						0sbeII-1ALL
751	Y R E W A P G A H S A L V G D F N N W N P N A D T M T R D D Y G V W E I F L P N N A D G S P A I P					Wheat SBEII-2

Fig. 11(ii).

H G S K V K F R F D T P S G V W V D S I P A W I K Y A V Q T A G E I G A P Y D G I H Y D P P S E E K Majority
 260 270 280 290 300
 H N S K V K F R F H - H G V W V E Q I P A W I R Y A T V T A S E S G A P Y D G L H W D P P S S E R TASBE102
 H N S K V K F R F H R G D G L W V D R V P A W I R Y A T F D A S K F G A P Y D G V H W D P P S G E R TASBEI
 H G S R V K V R M D T P S G I - K D S I P A W I K Y S V Q T P G D I - - P Y N G I Y Y D P P E E E K OsbeII-1ALL
 H G S R V K I R M D T P S G V - K D S I S A W I K F S V Q A P G E I - - P F N G I Y Y D P P E E E K Wheat SBEII-2
 Y V F K H P Q P K K P D S L R I Y E A H V G M S G P E P E I N T Y A E F R D E V L P R I K A L G Y N Majority
 310 320 330 340 350
 Y V F N H P R P P K P D V P R I Y E A H V G V S G G K L E A G T Y R E F P D N V L P C L R A T N Y N TASBE102
 Y V F K H P R P R K P D A P R I Y E A H V G M S G E K P E V S T Y R E F A D N V L P R I K A N N Y N TASBEI
 Y V F K H P Q P K R P K S L R I Y E T H V G M S S P E P K I N T Y A N F R D E V L P R I K R L G Y N OsbeII-1ALL
 Y V F Q H P Q P K R P E S L R I Y E S H I G M S S P E P K I N S Y A N F R D E V L P R I K R L G Y N Wheat SBEII-2
 A V Q L M A I Q E H S Y Y A S F G Y H V T N F F A V S S R S G T P E D L K S L I D K A H S L G L R V Majority
 360 370 380 390 400
 T V Q L M G I M E H S O S A S F G Y H V T N F F A V S S R S G T P E D L K Y L I D K A H S L G L R V TASBE102
 T V Q L M A I M E H S Y Y A S F G Y H V T N F F A V S S R S G T P E D L K Y L V D K A H S L G L R V TASBEI
 A V Q I M A I Q E H S Y Y G S F G Y H V T N F F A P S S R F G S P E D L K S L I D R A H E L G L V V OsbeII-1ALL
 A V Q I M A I Q E H S Y Y A S F G Y H V T N F F A P S S R F G T P E D L K S L I D R A H E L G L I V Wheat SBEII-2
 L M D V V H S H A S N N T L D G L N G F D V G Q G T D T S Y F H G G X R G H H K M W D S R L F N Y G Majority
 410 420 430 440 450
 L M D V V H S H A S N N V I D G L N G Y D V G Q S A H E S Y F Y T G D K G G Y N K M W N G R M F N Y A TASBE102
 L M D V V H S H A S N K T D G L N G Y D V G Q N T Q E S Y F H I G E R G Y H K L W D S R L F N Y A TASBEI
 L M D V V H S H A S N N T L D G L N G F D - - - G T D T H Y F H G G S R G H H W M W D S R V F N Y G OsbeII-1ALL
 L M D I V H S H S S N N T L D G L N G F D - - - G T D T H Y F H G G P R G H H W M W D S R L F N Y G Wheat SBEII-2
 N W E V L R F L L S N A R Y W L D E F K F D G F R F D G V T S M L Y T H H G L N M S F T G S Y K E Y Majority
 460 470 480 490 500
 N W E V L R F L L S N L R Y W M D E F M F D G F R F V G V T S M L Y N H N G I N M S F N G N Y K D Y TASBE102
 N W E V L R F L L S N L R Y W M D E F M F D G F R F D G V T S M L Y N H H G I N M S F A G S Y K E Y TASBEI
 N K E V I R F L L S N A R W W L E E Y K F D G F R F D G A T S M M Y T H H G L Q V T F T G S Y H E Y OsbeII-1ALL
 S W E V L R F L L S N A R W W L E E Y K F D G F R F D G V T S M M Y T H H G L Q M T F T G N Y G E Y Wheat SBEII-2

Fig. 17 (iii).

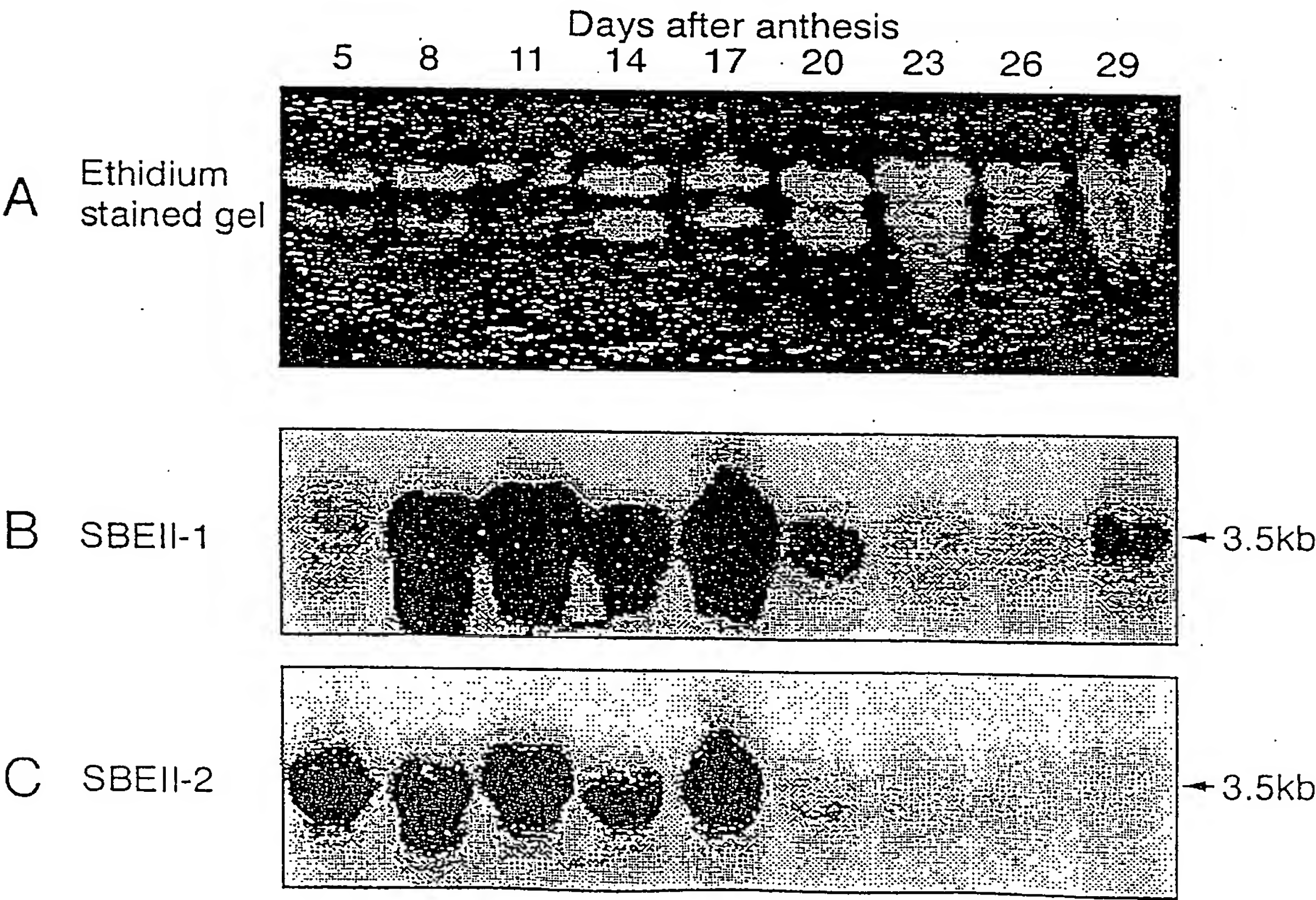
i).

	F	G	L	A	T	O	V	D	A	V	V	Y	L	M	L	A	N	D	L	I	H	G	L	X	P	E	A	V	V	V	G	E	D	V	S	G	M	P	V	L	C	X	P	V	D	E	G	G	V	G	550	Majority																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																											
1348	I	G	L	O	T	N	V	D	A	F	V	M	M	L	A	N	H	L	M	H	K	L	F	P	E	A	I	V	V	A	V	D	V	S	G	M	P	V	L	C	W	P	V	D	E	G	G	L	G	540	TASBE102																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																												
1324	F	G	L	O	T	D	V	D	A	V	V	Y	L	M	L	A	N	H	L	M	H	K	L	L	P	E	A	T	V	V	A	E	D	V	S	G	M	P	V	L	C	R	S	V	D	E	G	G	V	G	530	TASBEI																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																											
833	F	G	F	A	T	D	V	D	A	V	V	Y	L	M	L	M	N	D	L	I	H	G	F	Y	P	E	A	V	T	I	G	E	D	V	S	G	M	P	T	F	A	L	P	V	Q	V	G	G	V	G	520	OsbeII-1ALL																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																											
1633	F	G	F	A	T	D	V	D	A	V	V	Y	L	M	L	V	N	D	L	I	H	G	L	H	P	D	A	V	S	I	G	E	D	V	S	G	M	P	T	F	C	I	P	V	P	D	G	G	V	G	510	Wheat SBEII-2																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																											
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1498	F	D	Y	R	Q	A	M	T	I	P	D	R	W	I	D	Y	L	E	N	K	G	D	Q	Q	W	S	M	S	S	V	I	S	Q	T	L	T	N	R	R	Y	P	E	K	F	I	A	Y	A	E	S	590	TASBE102																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																											
1474	F	D	Y	R	L	A	M	A	I	P	D	R	W	I	D	Y	L	K	N	K	D	D	L	E	W	S	M	S	G	-	I	A	H	T	L	T	N	R	R	Y	T	E	K	C	I	A	Y	A	E	S	580	TASBEI																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																											
983	F	D	Y	R	L	H	M	A	V	A	D	K	W	I	E	L	K	G	N	D	E	-	A	W	E	M	G	N	I	V	-	H	T	L	T	N	R	R	W	P	E	K	C	V	T	Y	A	E	S	570	OsbeII-1ALL																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																												
1783	L	D	Y	R	L	H	M	A	V	A	D	K	W	I	E	L	K	Q	S	D	E	-	S	W	K	M	G	D	I	V	-	H	T	L	T	N	R	R	W	L	E	K	C	V	T	Y	A	E	S	560	Wheat SBEII-2																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																												
	H	D	Q	A	L	V	G	D	K	T	I	A	F	L	L	M	D	K	D	M	Y	D	G	M	A	L	X	X	P	S	S	P	T	I	D	R	G	I	A	L	Q	K	M	I	H	L	I	T	M	G	650	Majority																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																											
1648	Q	N	H	S	I	I	G	S	K	T	M	A	F	L	L	M	E	W	E	T	Y	S	G	M	S	A	M	D	P	D	S	P	T	I	D	R	A	I	A	L	Q	K	M	I	H	F	I	T	M	A	640	TASBE102																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																											
1621	H	D	Q	S	I	V	G	D	K	T	M	A	F	L	L	M	D	K	E	M	Y	T	G	M	S	D	L	Q	P	A	S	P	T	I	D	R	G	I	A	L	Q	K	M	I	H	F	I	T	M	A	630	TASBEI																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																											
1127	H	D	Q	A	L	V	G	D	K	T	I	A	F	W	L	M	D	K	D	M	Y	D	F	M	A	L	N	G	P	S	T	P	S	I	D	R	G	I	A	L	H	K	M	I	R	L	I	T	M	G	620	OsbeII-1ALL																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																											
1927	H	D	Q	A	L	V	G	D	K	T	I	A	F	W	L	M	D	K	D	M	Y	D	F	M	A	L	D	R	P	S	T	P	R	I	D	R	G	I	A	L	H	K	M	I	R	L	V	T	M	G	610	Wheat SBEII-2																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																											
	L	G	G	D	G	Y	L	N	F	M	G	N	E	F	G	H	P	E	W	I	O	F	P	R	G	P	Q	-	L	P	T	G	K	-	-	P	G	N	N	S	Y	D	K	C	R	R	R	F	D	700	Majority																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																												
11798	F	G	G	D	S	Y	L	K	F	M	G	N	E	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-

Fig.11A.

		Percent Similarity					
Percent Divergence		1	2	3	4		
	1		63.9	31.2	37.0	1	TASBE1D2
	2	39.1		46.7	41.8	2	TASBEI
	3	86.9	73.8		69.6	3	sbell-1ALL
	4	94.5	76.4	25.3		4	Wheat SBELL-2
		1	2	3	4		

Fig.12.



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Fig.13.

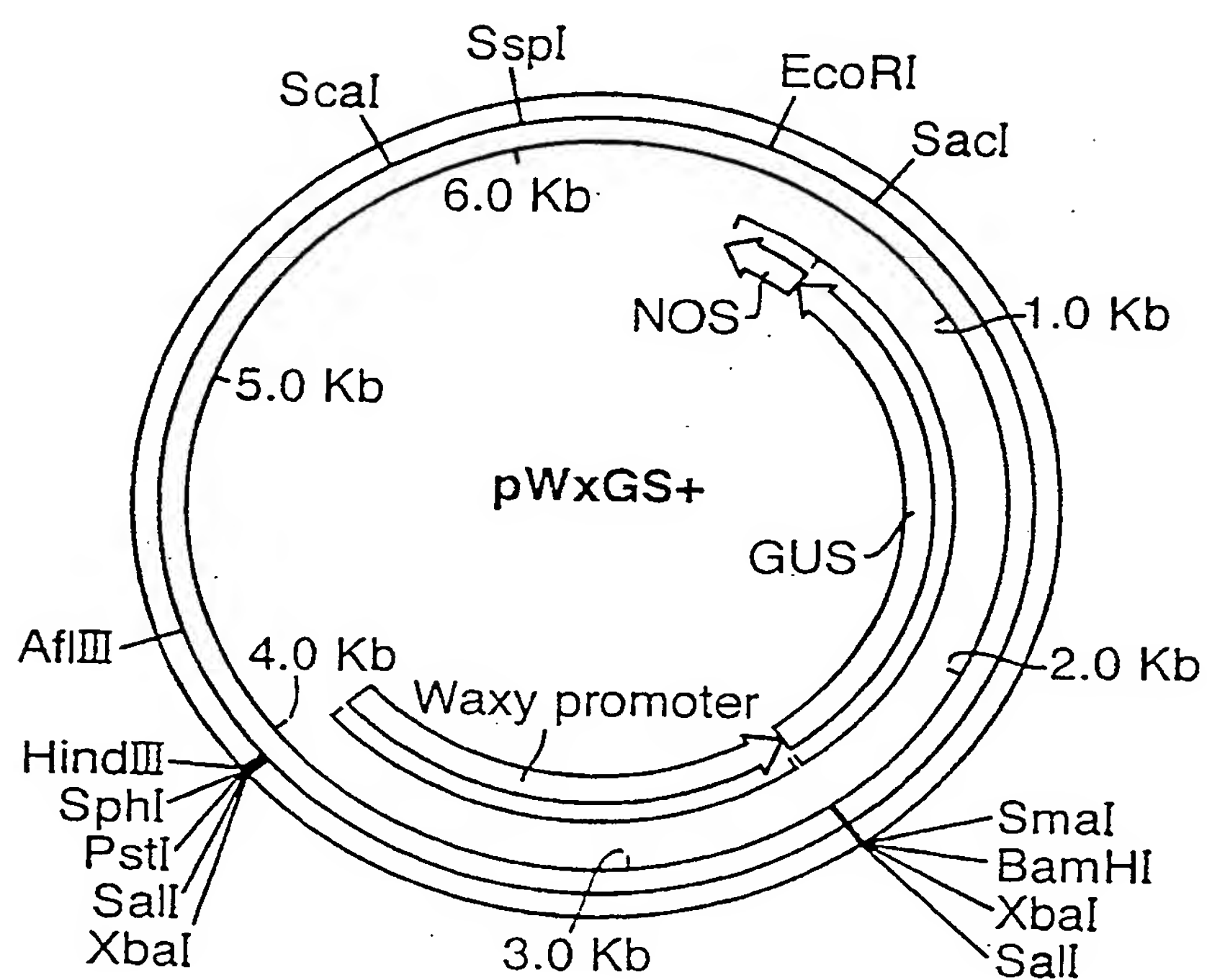


Fig.13A.

10 20 30 40 50 60 70
AAGCTTGCATGCCCTGCAGGTCGACTCTAGACCAAAATTTCATGGTAGTTGGAGCCTACCCAGATTTCATG 70
ATTAACTGTGCTATTGAAATTGTTGAAAAATGGTTGTCTGTCTGTCGTATCCGACGGATAACGGAAACCCGTCC 140
GAAATTCAATGGGCATAGATATAGATTGTACCCACTACTAGTATGGTCGCAGGCGGATATTGG 210
TTGCAACCGCAGATATAGTTTCGGGGAAAGGATTAGGCTCAGCTCCATCCCTAGACCCCACTTGTGTGT 280
GTGGGGGGTCTACCCCTTCAAAAGGAAATACTACACACAGTGCATATAAGAGATGAATATTCCAAA 350

360 370 380 390 400 410 420
ATTCAGCAGTCAAGAAGCCCTGATAAACTGTCTGGCATAAGCTAGTACTTTATACACTTCAAGACCAAAAG 420
AAATCACTAAGTACAGATTTTAGTGACTCGTAAGTACAGATATCATCTTACAAAGGCCAGCCAGCGACC 490
TATTACACAGCCCGCTCGGGCCCGGACGTCGGGACACATCTTCTTCCCTTTTGGTGAAGCTCTGCTC 560
GCAGCTGTCCGGCTGCTTGGACGTTTCGTGGCAGATTTCATCTGCTCCTGCTCCTGCTTCCCTGGG 630
TAGCTTGTGCAGTGGAGCTGACATGGTCTGAGCAGGCTTAAAAATTGCTCGTAGACGAGGATACCAGCA 700

710 720 730 740 750 760 770
CAGCACGTTGCGGATTCTCTGCTGTGAAGTGCAACGTCTAGGATTGTCAACGCCCTTGGTCGCGTCGA 770
TGCCGGTGGTGAGCAGAGCAGCAACAGCTGGGCGGCCCAAGTTGGCTTCCGTGTCTTCGTCTGTACGTACG 840
CGCGCGCCGGGACACGCAGAGAGCGGAGAGCCGTGCACGGGAGGTGTTGCAAGTGCAGCCG 910
CGCGCCCGCGCCCGGTGGGCAACCCAAAAGTACCCACGACAAGCGGCCCAAGCGATCC 980
AAGCTCCGGAACGCATCAGCCACAAGCAGCCGAGAACCGGTGGGCGACGCTCGTGGGACGGACG 1050

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Fig.13A(Cont).

1060	1070	1080	1090	1100	1110	1120
CGGGCAGCGCTTCCAAACGGGGCCACGTACGCCCGCGTGTCCGTGCGTGCGAGACGACAGCCAAGG	1120					
CGAGGCAGCCCCCGATCGGGAAAGCGTTTGGGGCGGAGCGCTGGCGTGCGGTGCTGCTGCTGCGCA	1190					
GTGCCGGGGGAACGGGTATCGTGGGGCGGCGGAGAGAGCGTGCGGAGGCCGAGAGCAGCGCGCG	1260					
GCCGGGTCACGCAACGCGCCCCACGTACTGCCCTCCCGCGCTAGAAATACCGAGGCCCTGGA	1330					
CCGGGGCCCCCGTCACATCCATCCATCGATCGCCACAGCCACACCCCGCGAGGCG	1400					
1410	1420	1430	1440	1450	1460	1470
ACGCGACAGCCGCGAGGAGGAATAAATCACTGCCAGCCAGTGAAGGGGAGAGTGTACTGCTCC	1470					
GTCGACTCTAGAGGATCC	1488					

(SEQ ID NO:55)

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Fig.13.

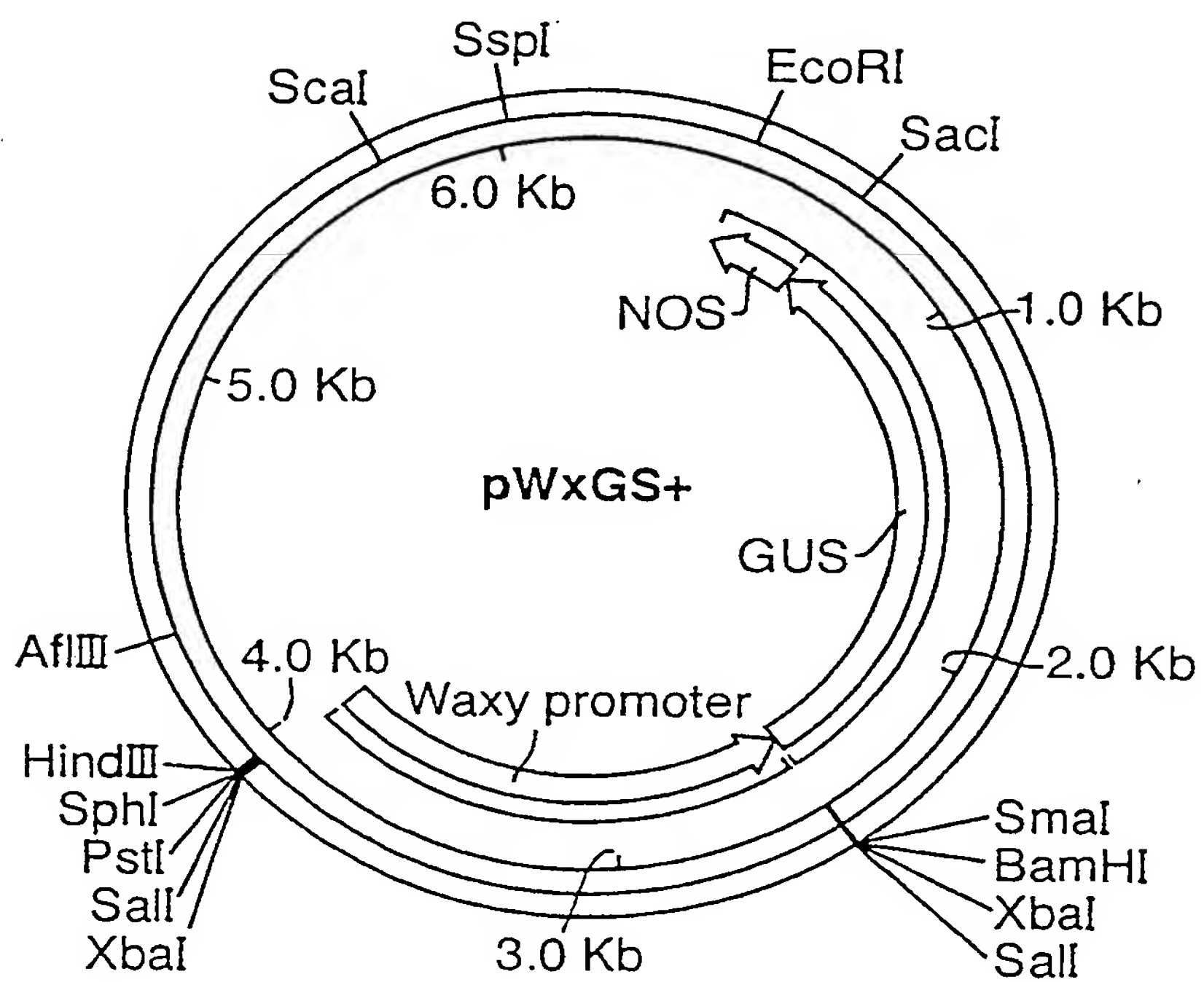


Fig.14.

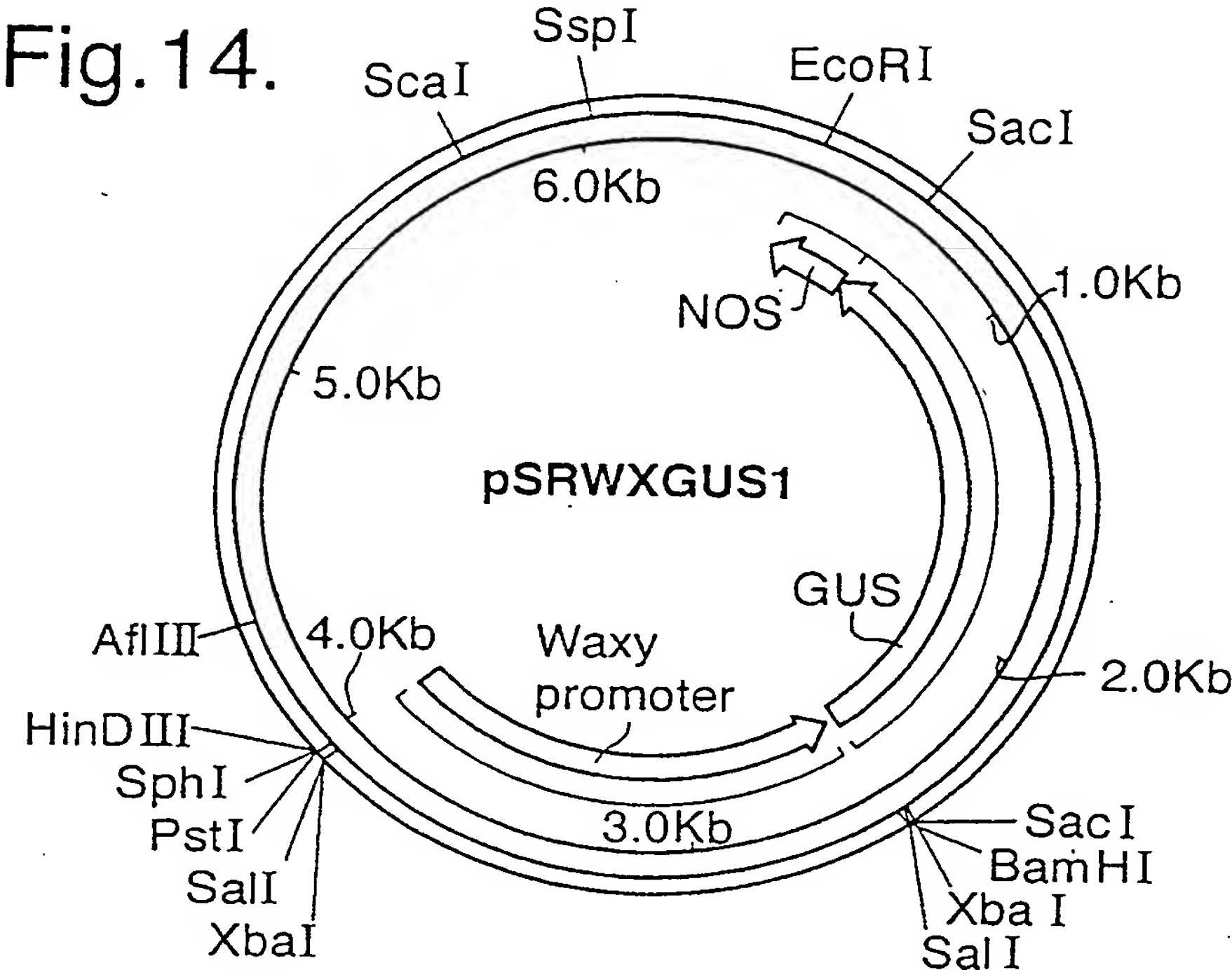


Fig.15.

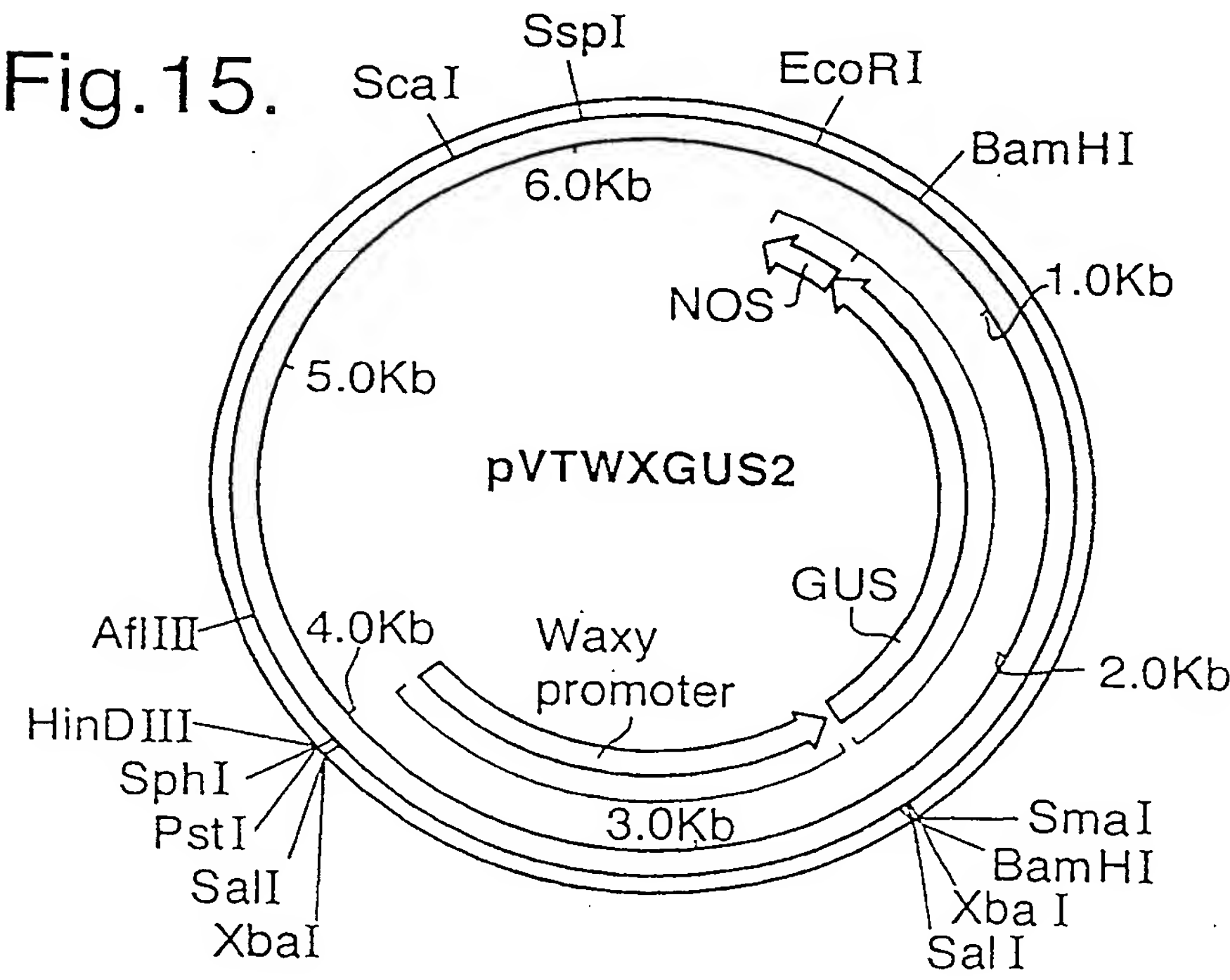


Fig.16.

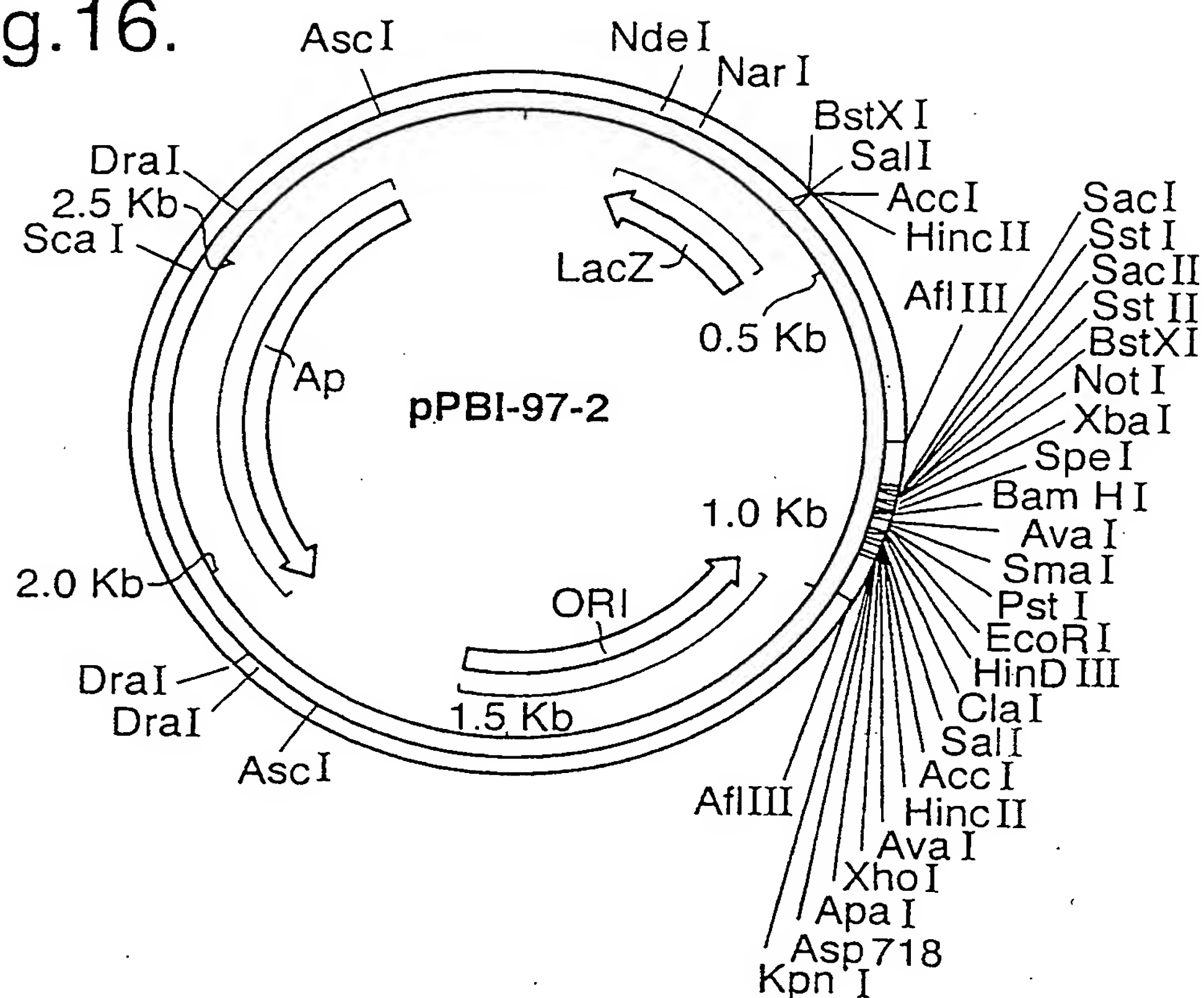


Fig.17.

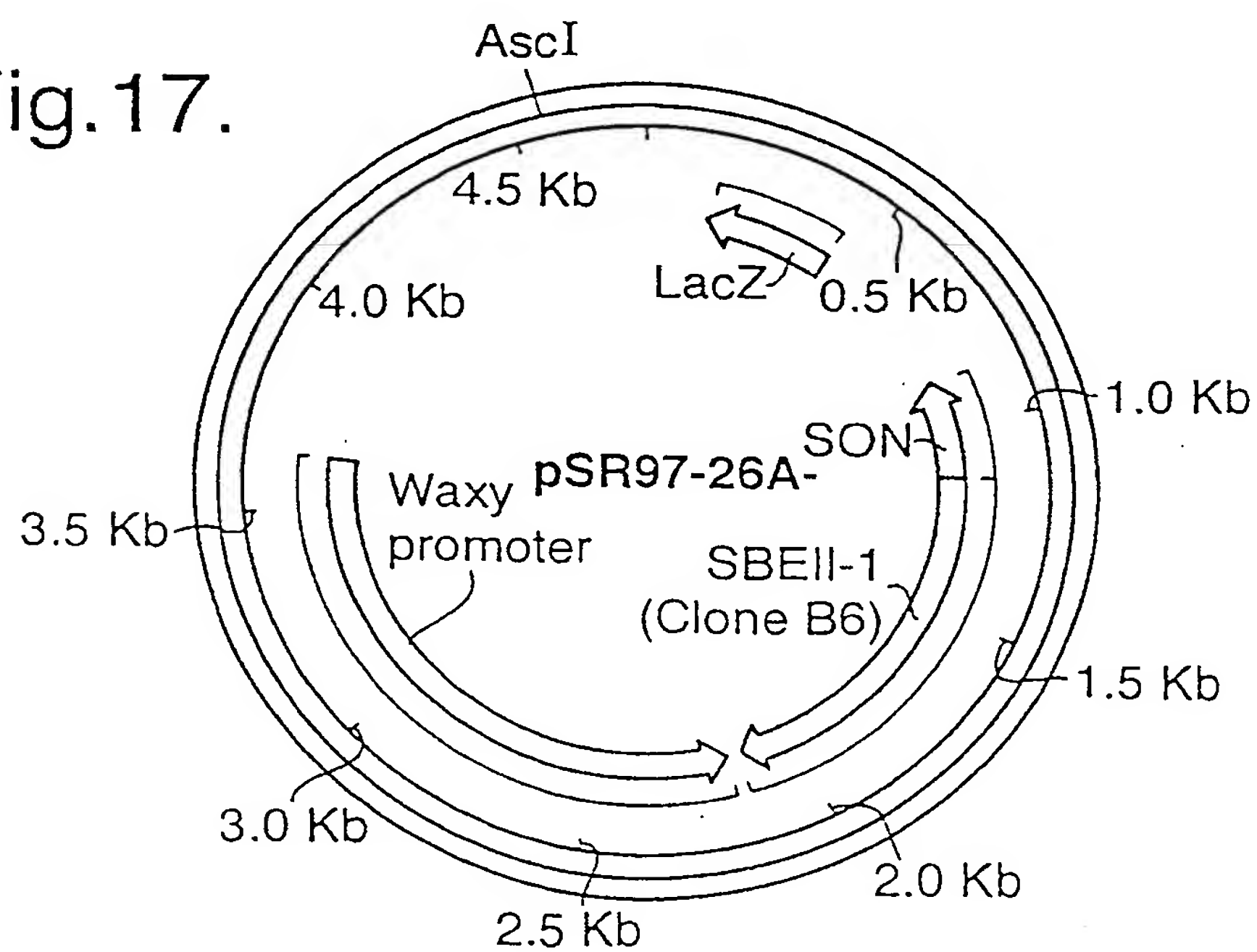


Fig.18.

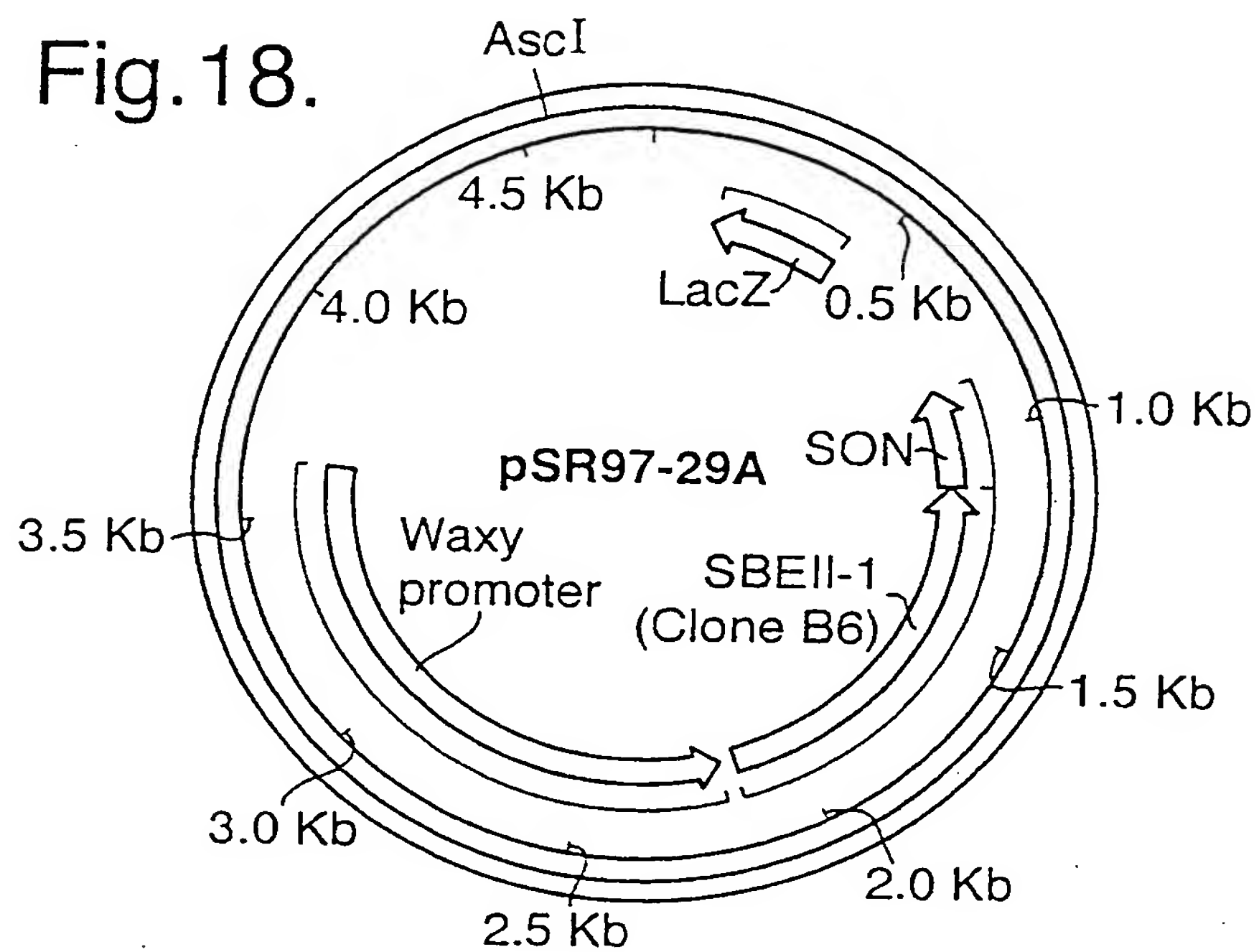
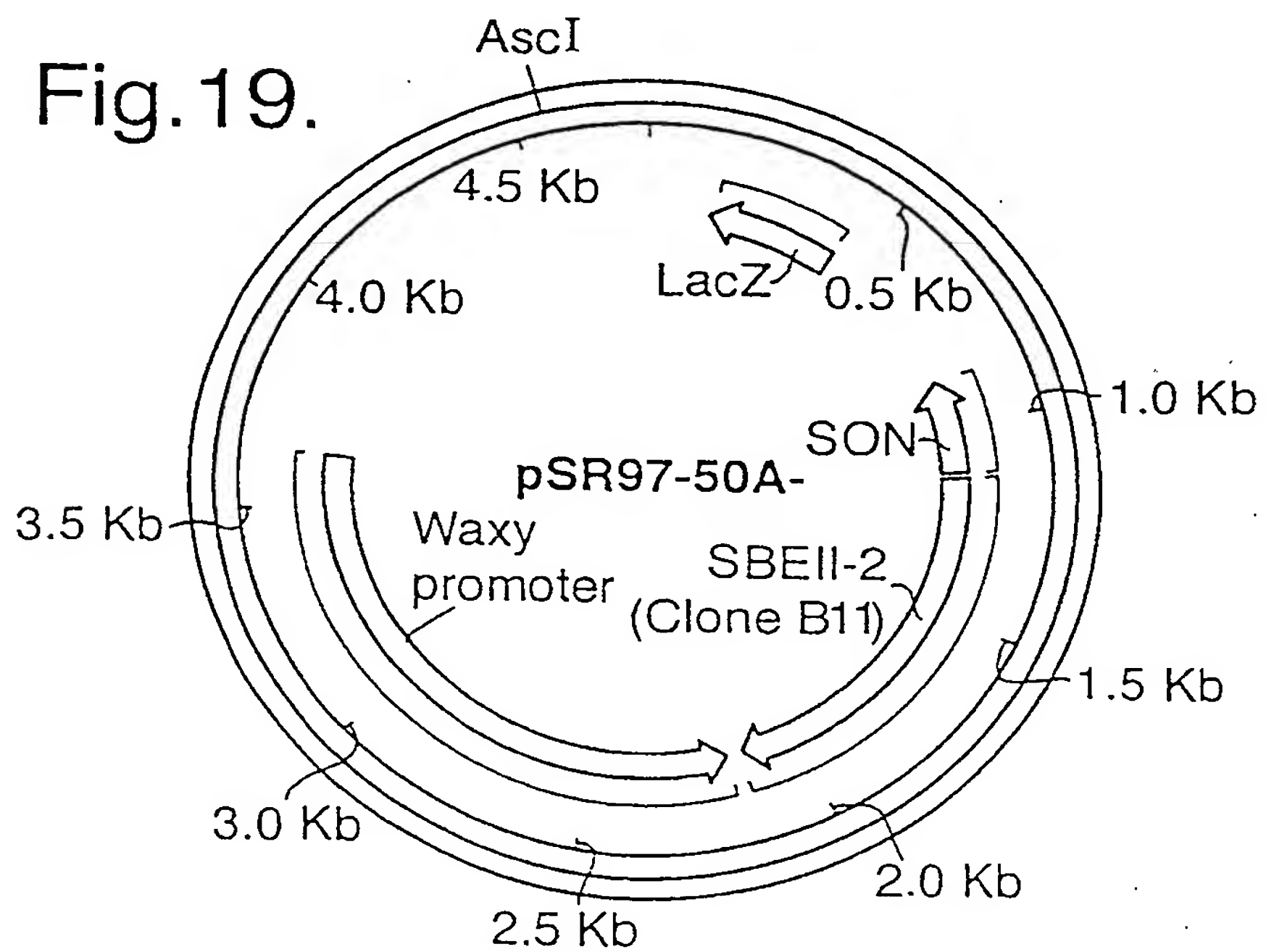


Fig.19.



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Fig.20.

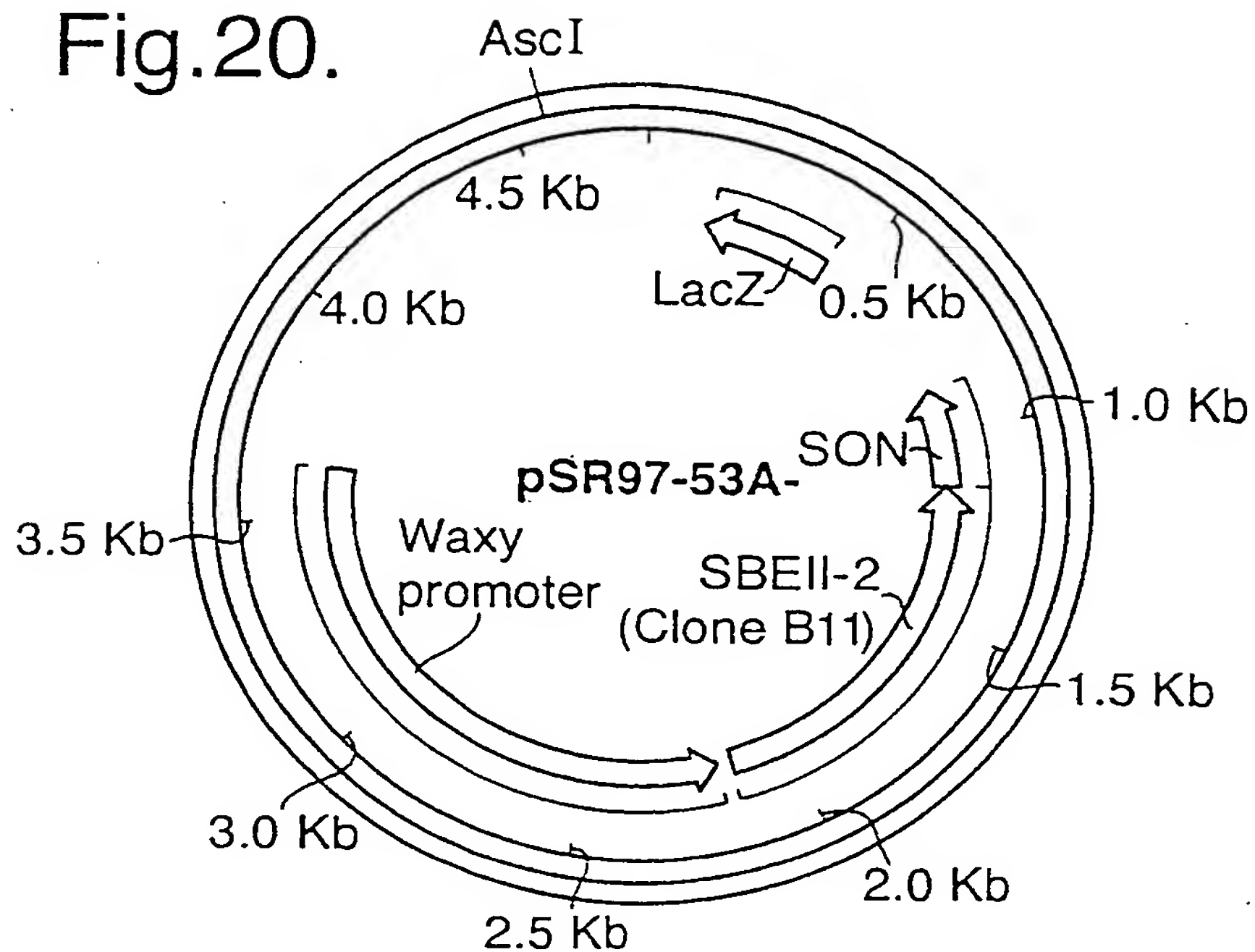


Fig.21.

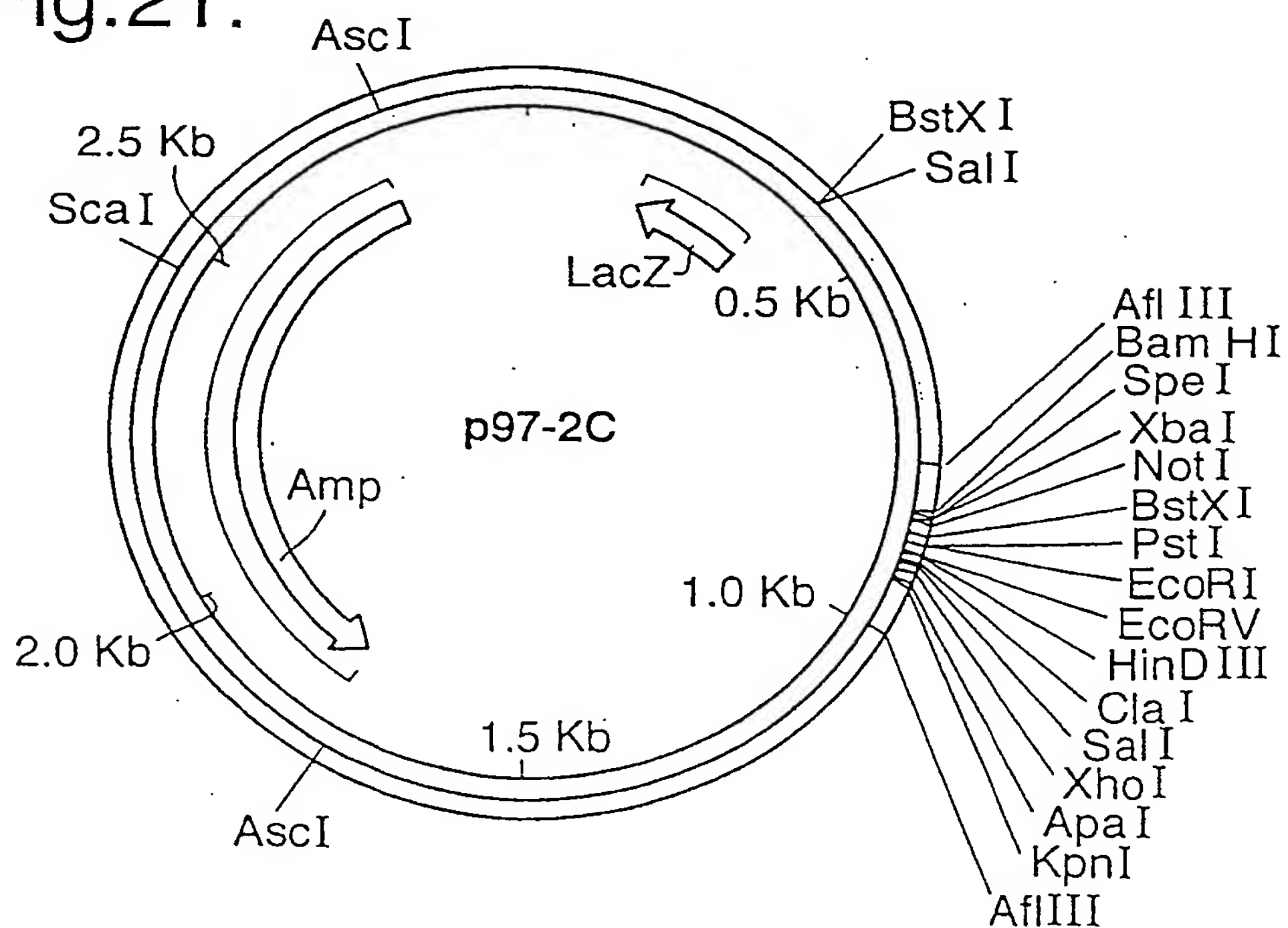


Fig.22.

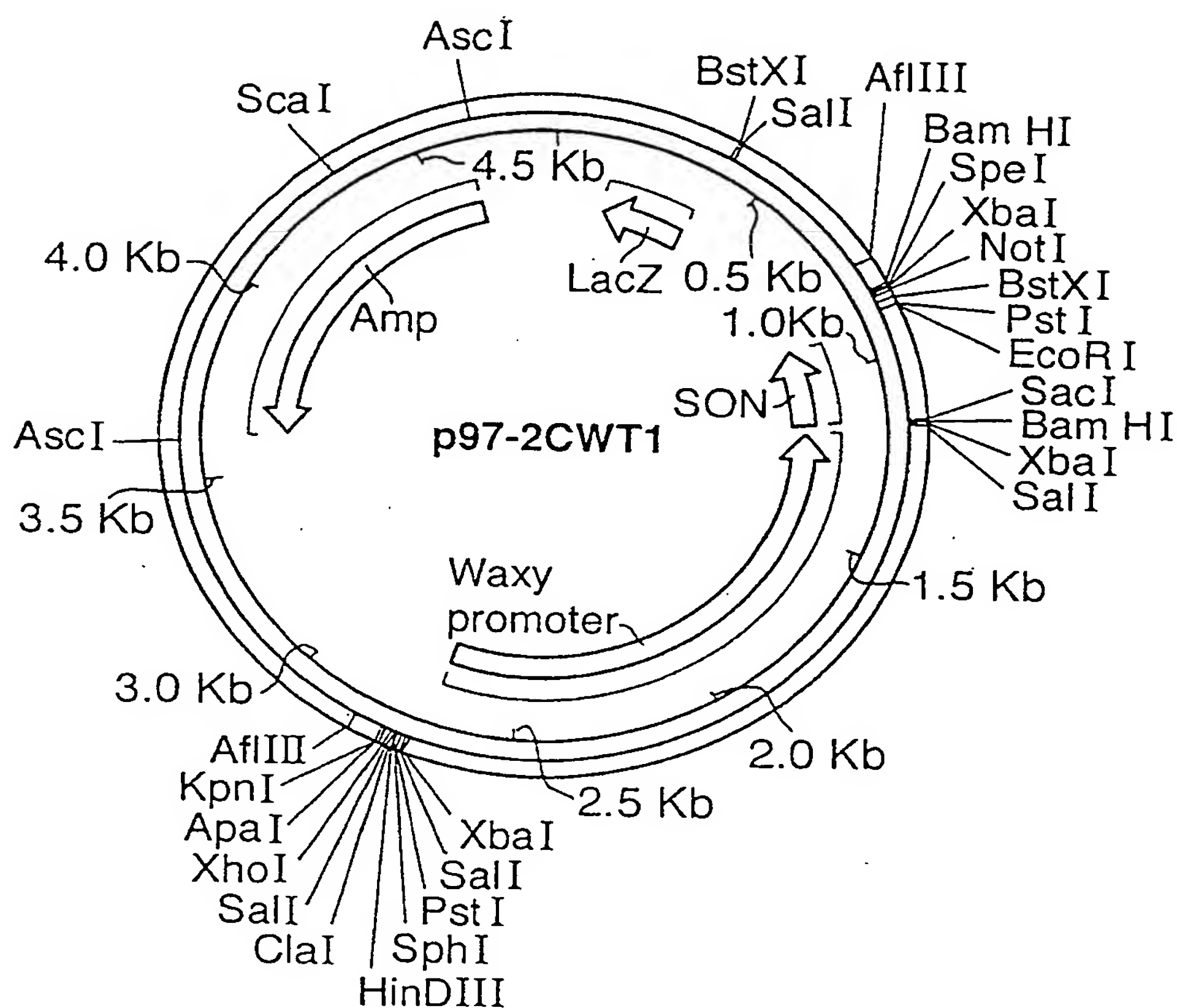


Fig.23.

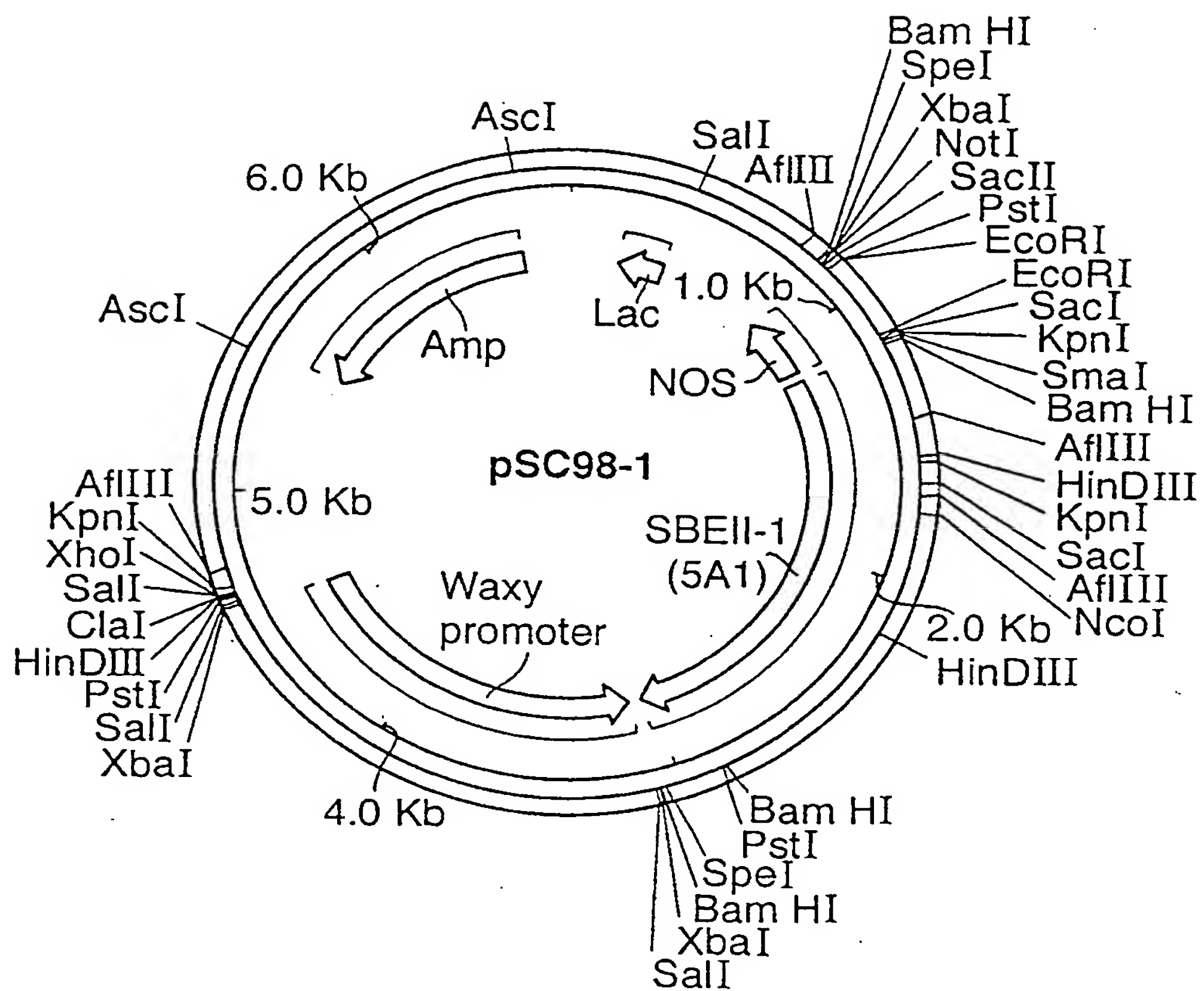


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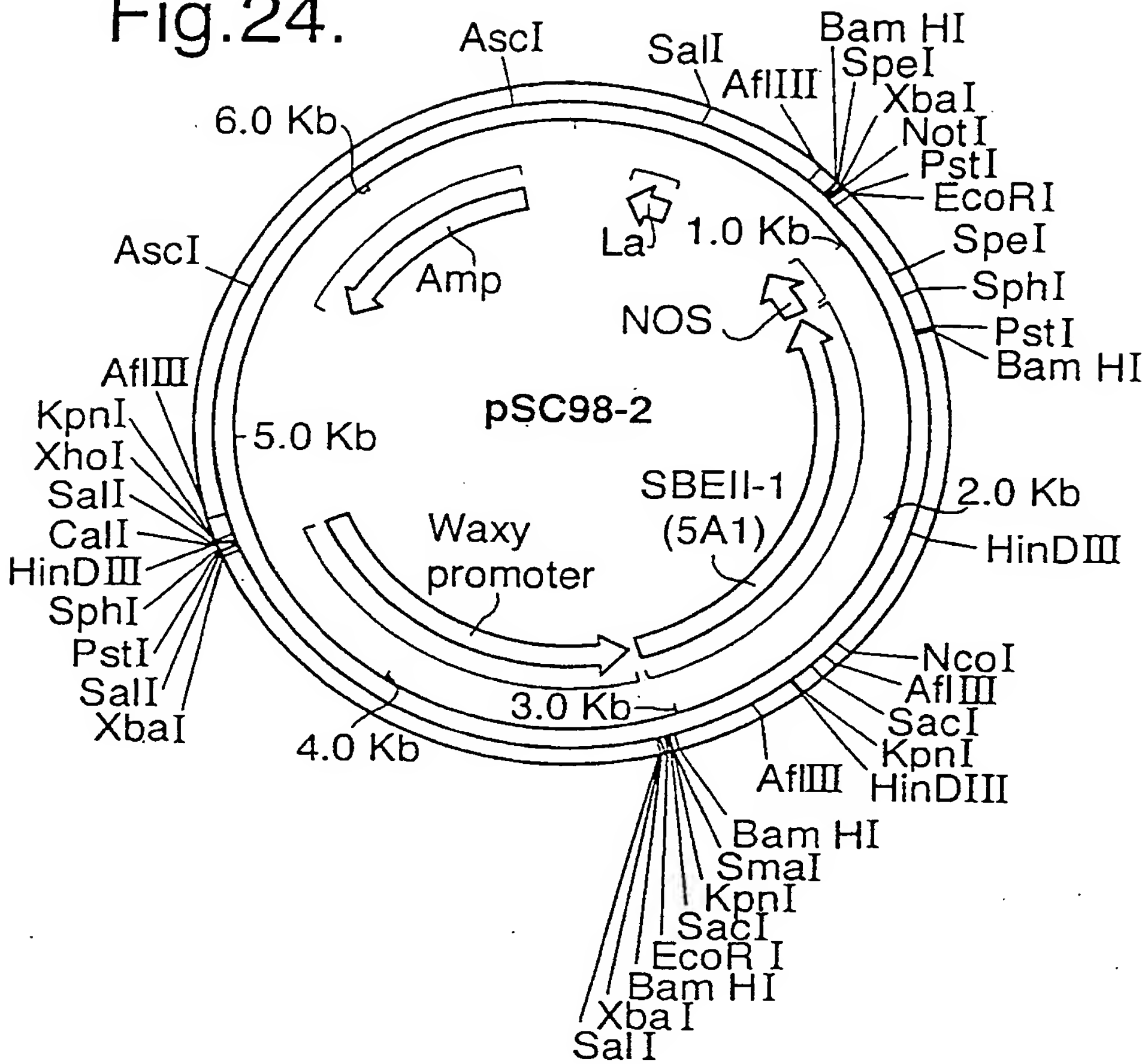
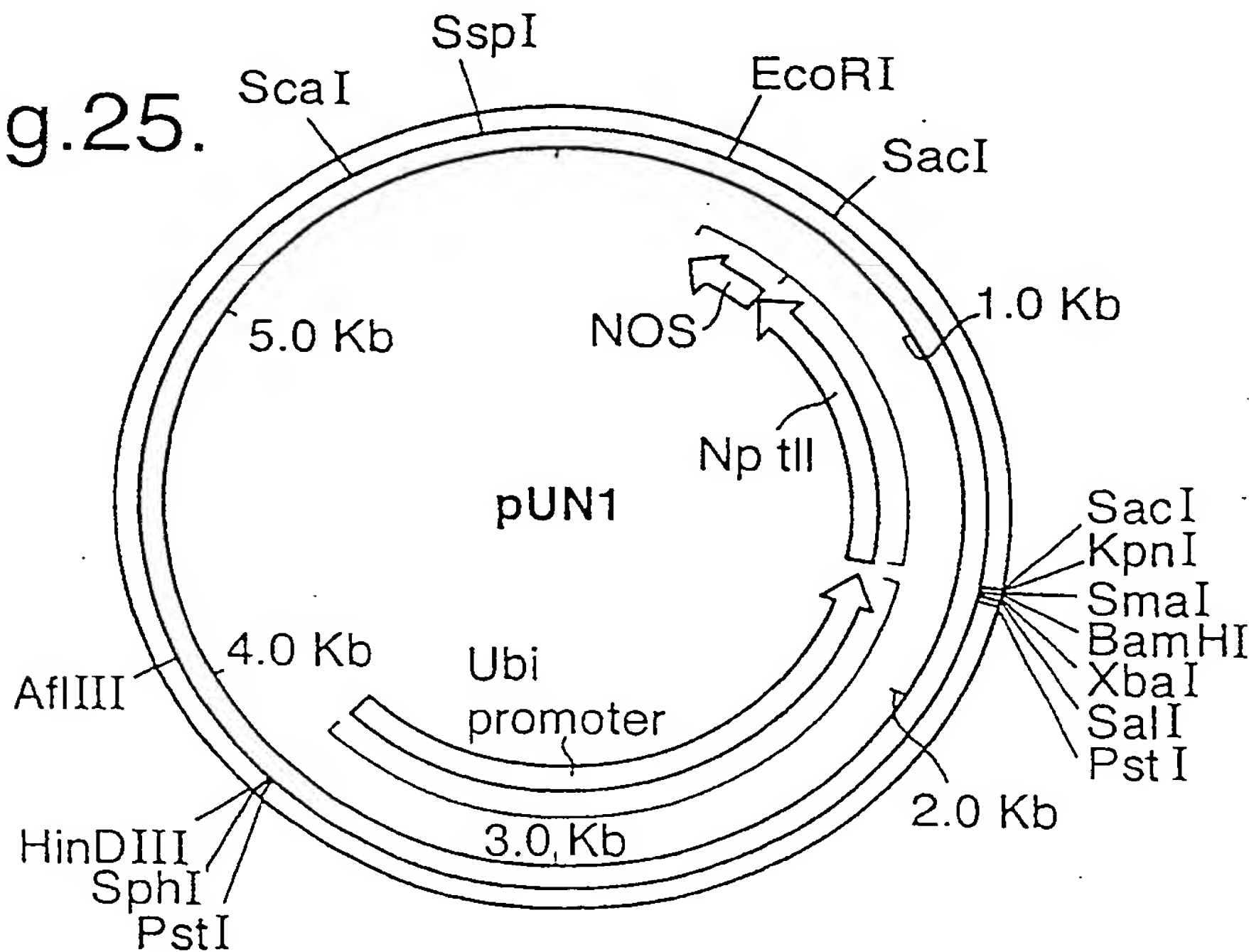


Fig.25.



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Fig.26.

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310 320 330 340 350 360
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ACCGCTATCA GGACATAGCG TTGGCTACCC GTGATATTGC TGAAGAGCTT GGCGGCGAAT 720
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Fig.27.

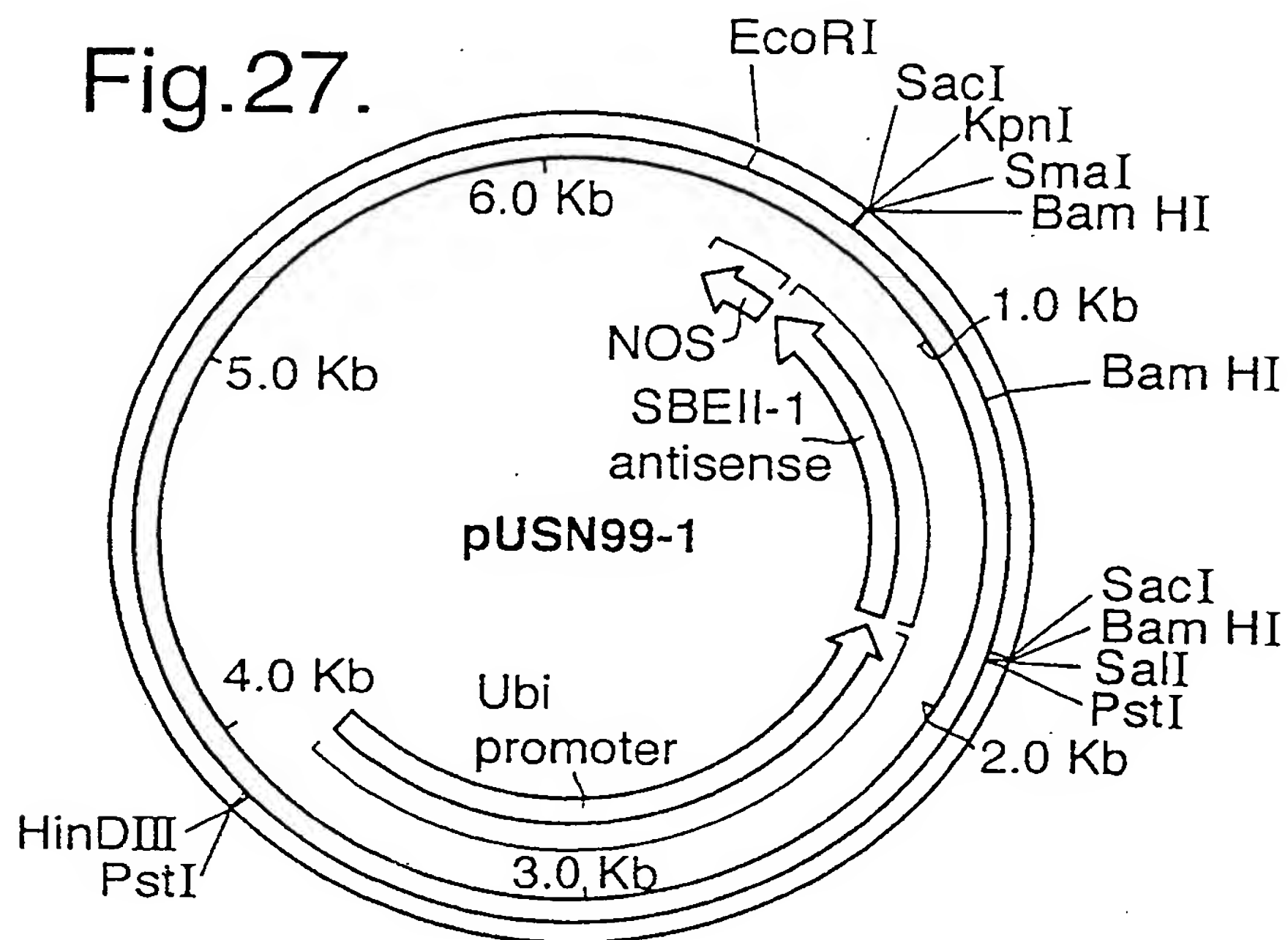
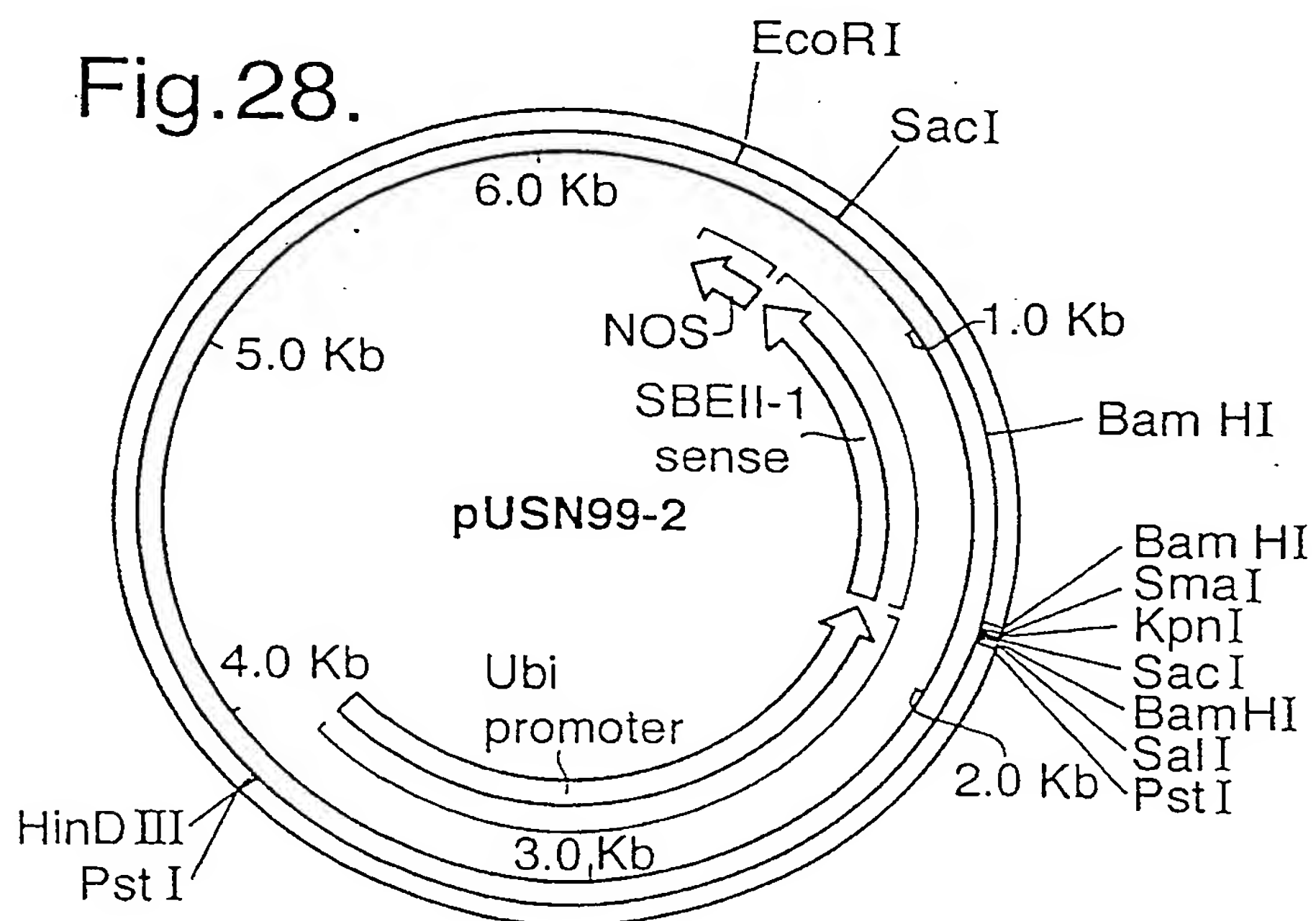
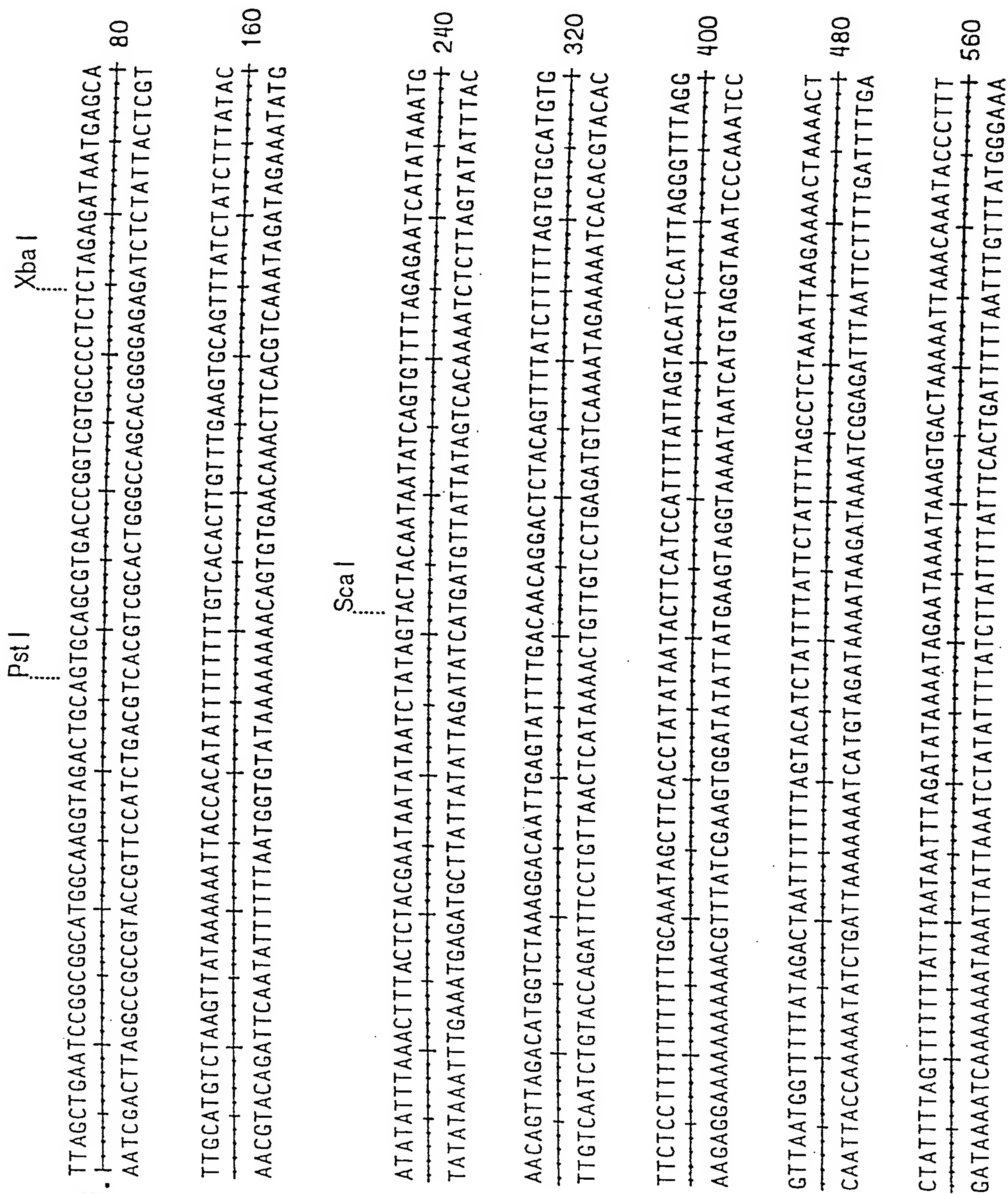
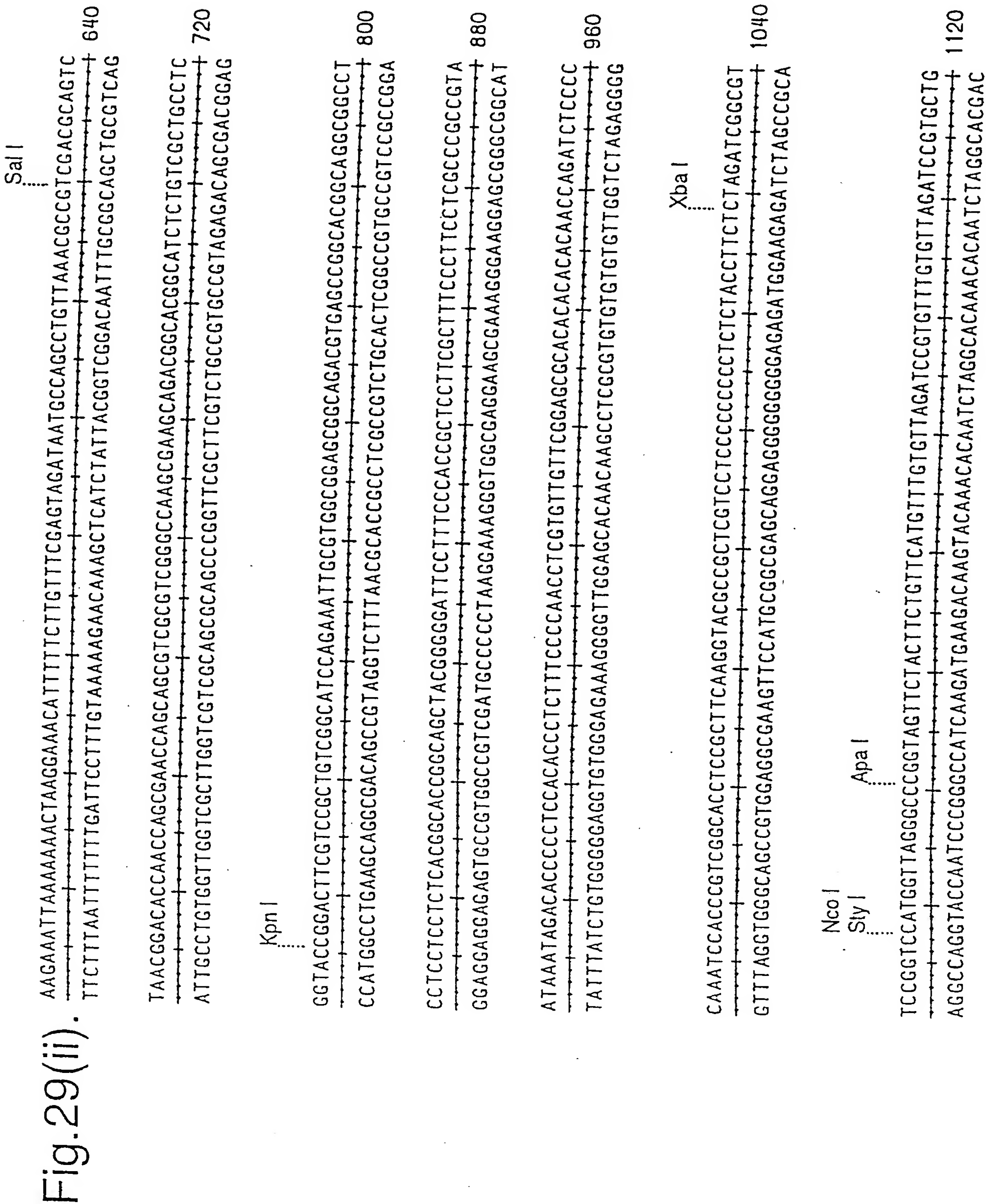


Fig.28.



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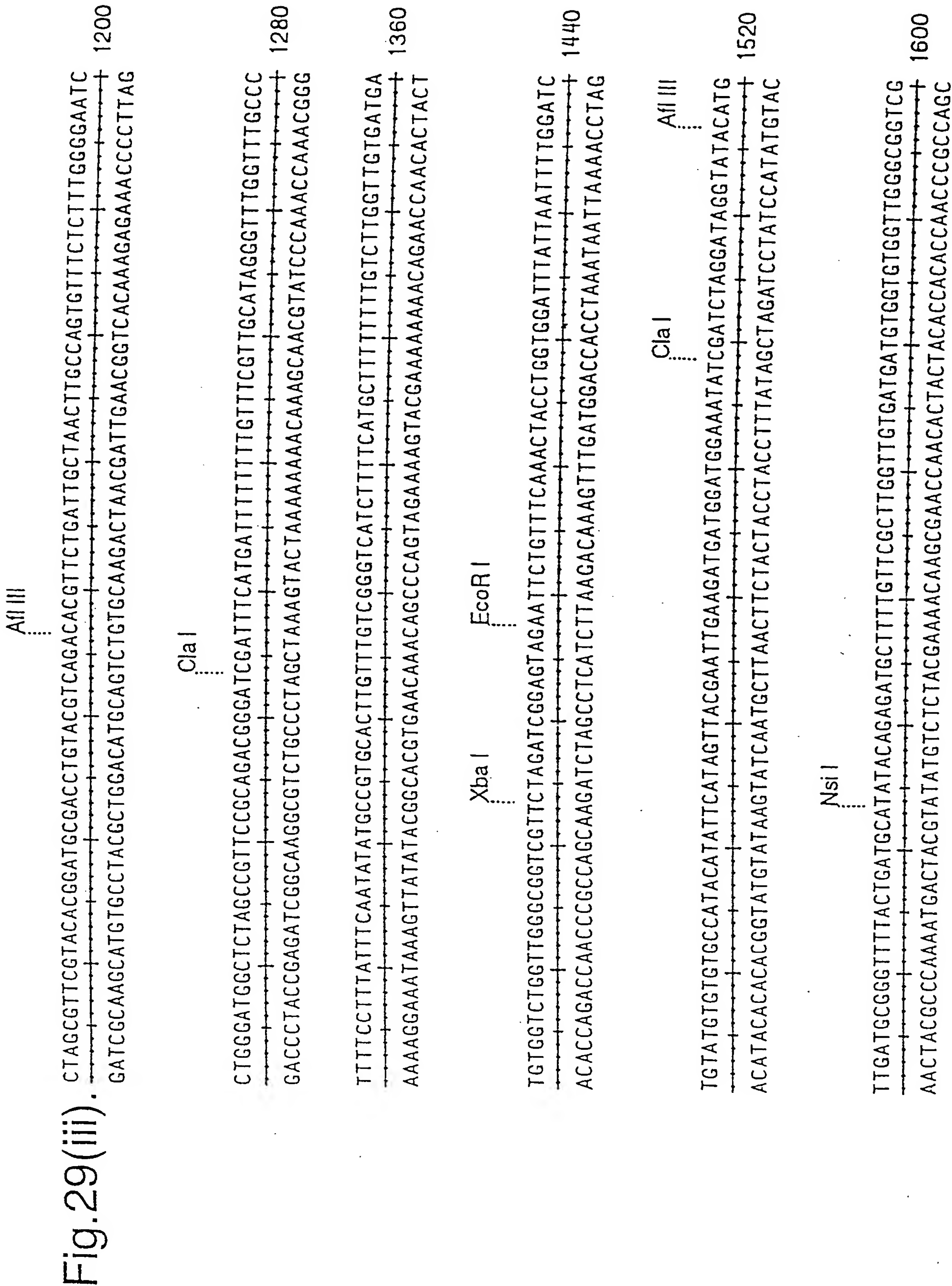


Fig.29(iv).

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1680

Cla I

Afl III

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1760

Nsi I

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1840

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1920

Pst I

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2000

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2038 (SEQ ID No : 52)

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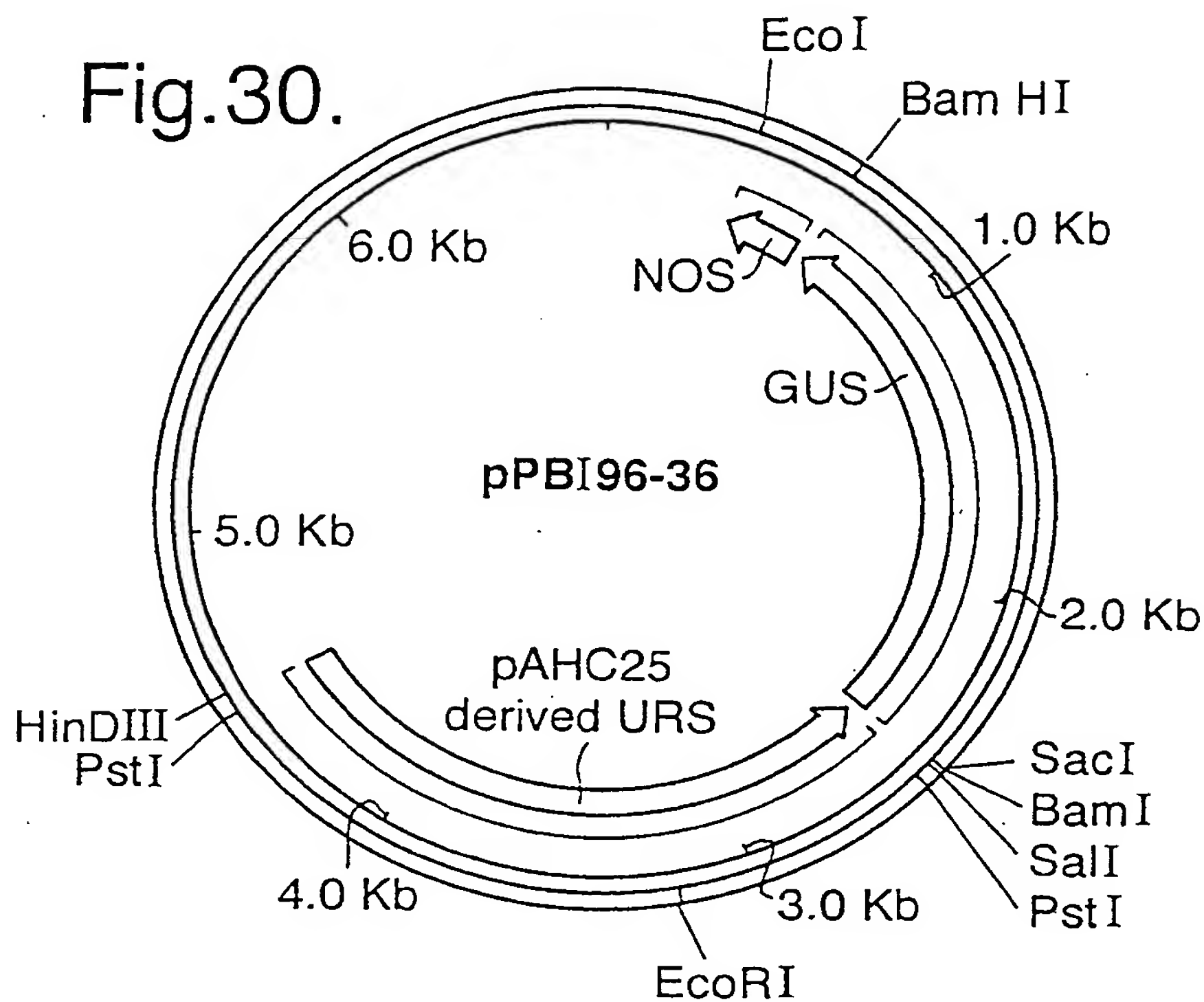


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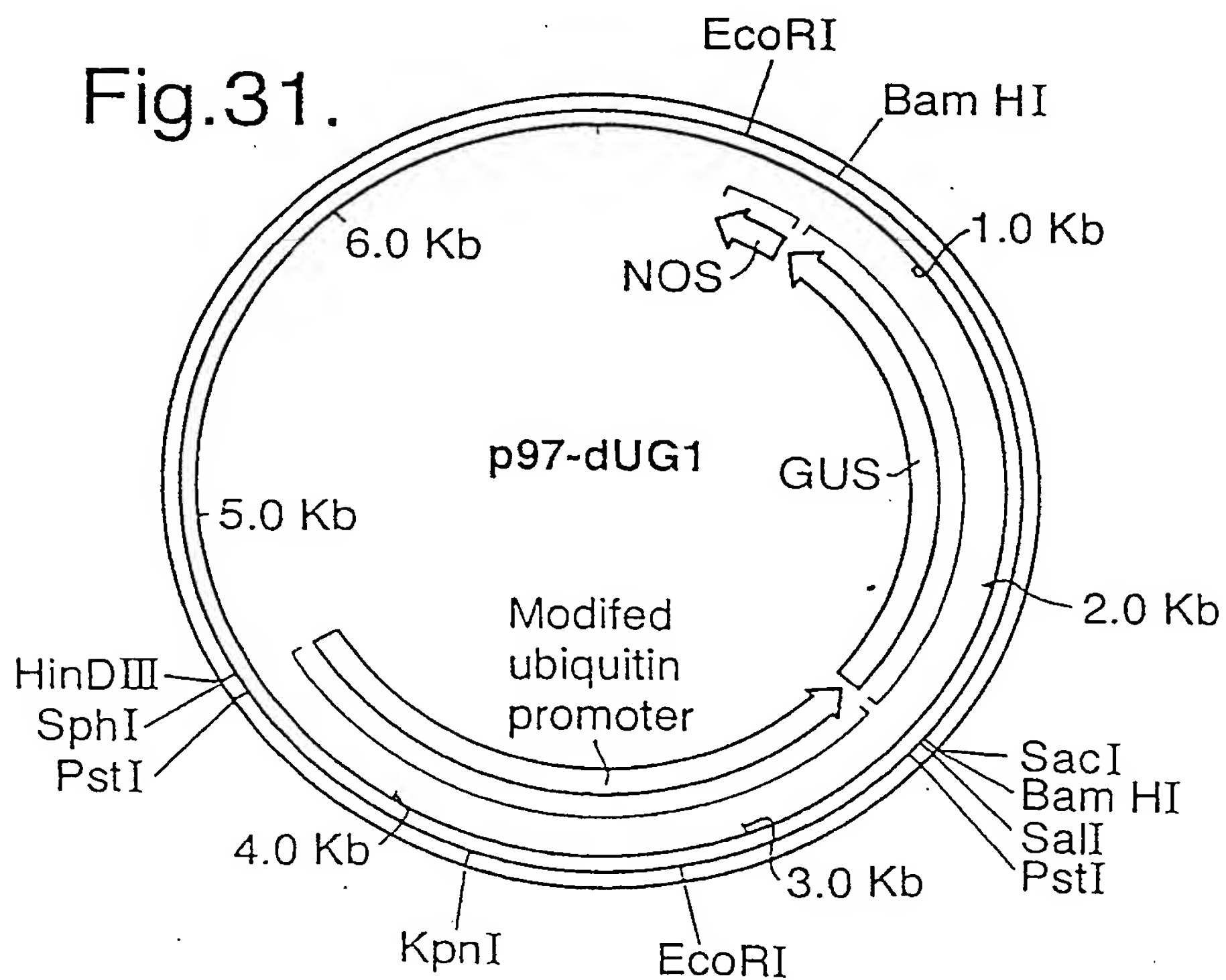


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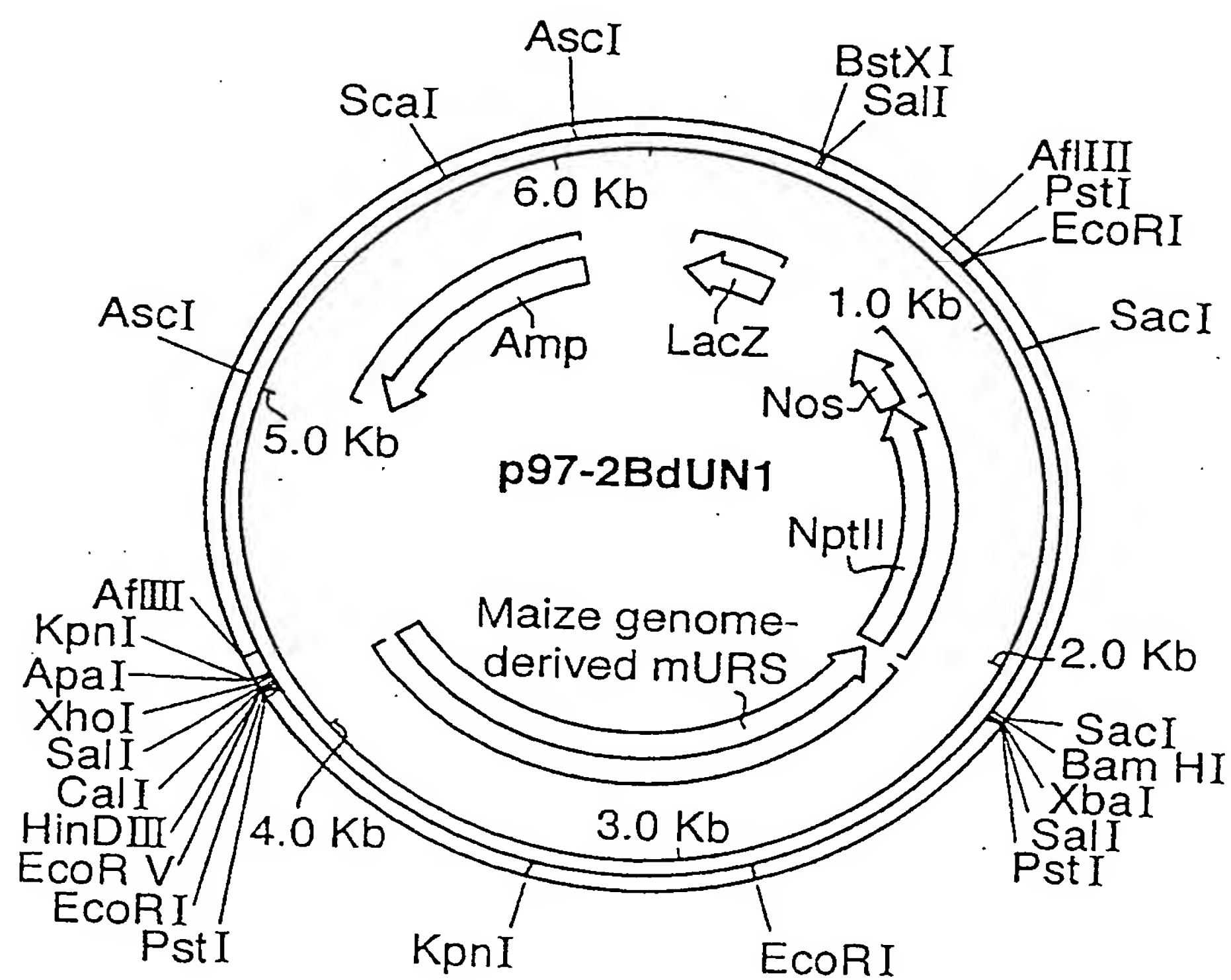


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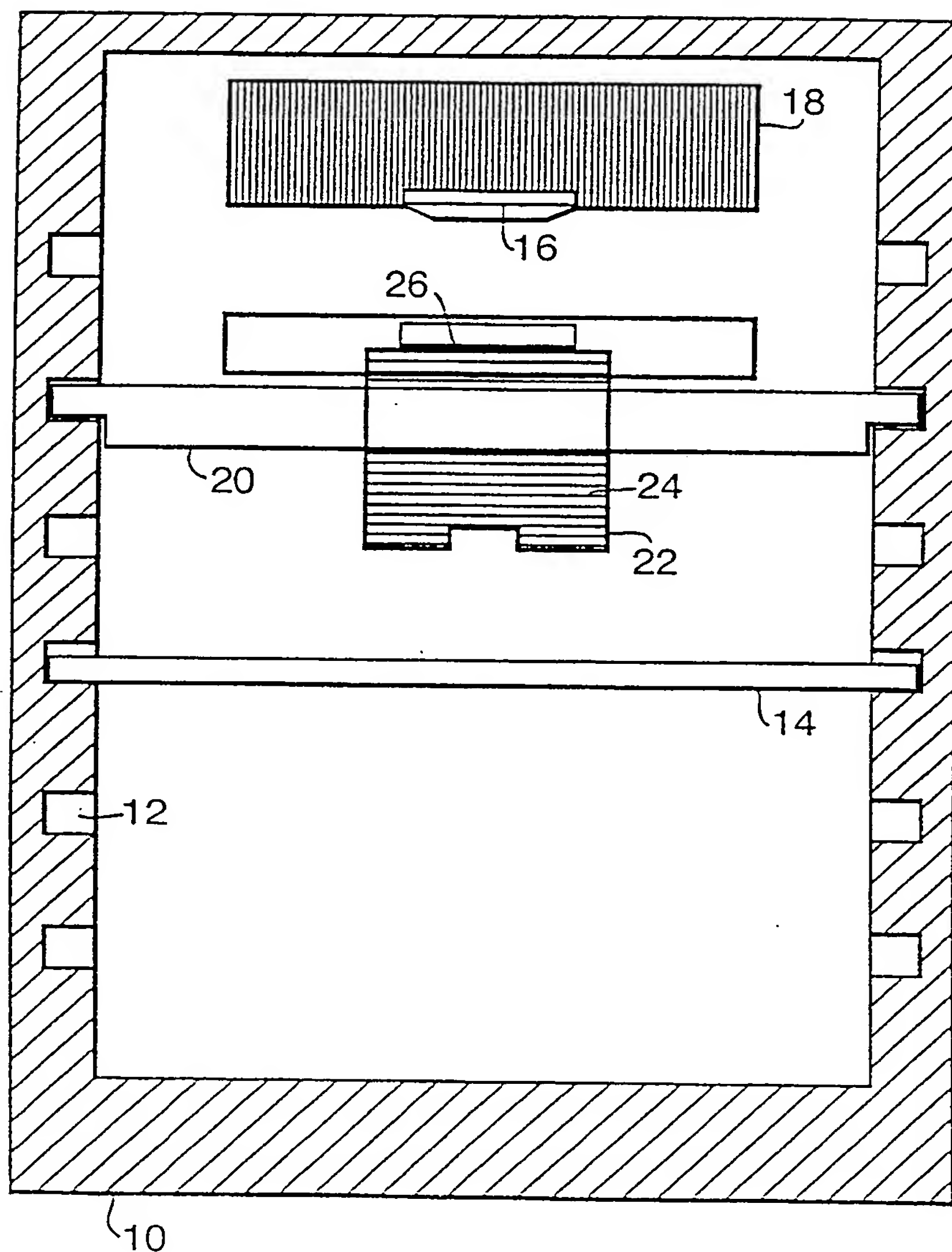
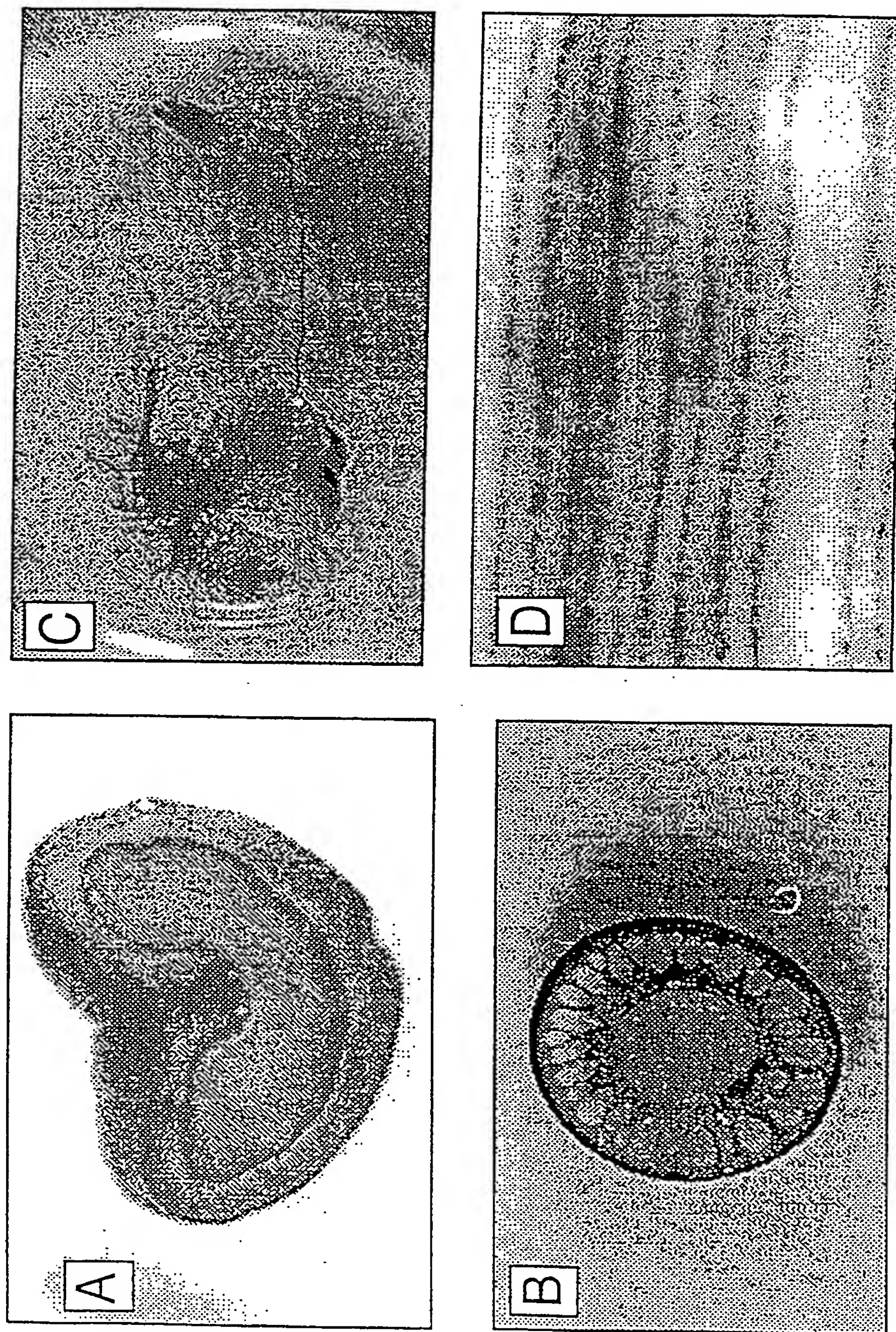


Fig.34.



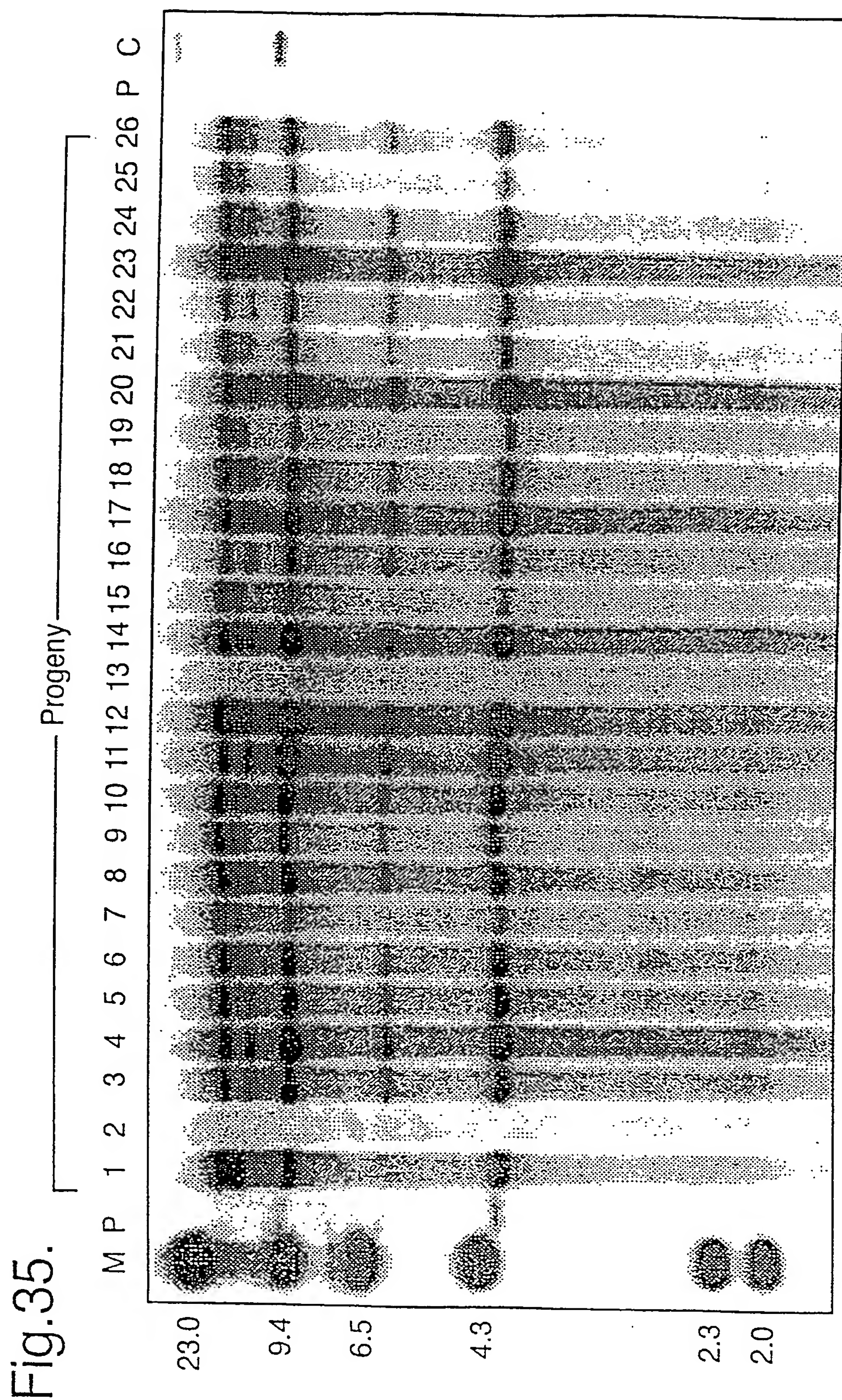


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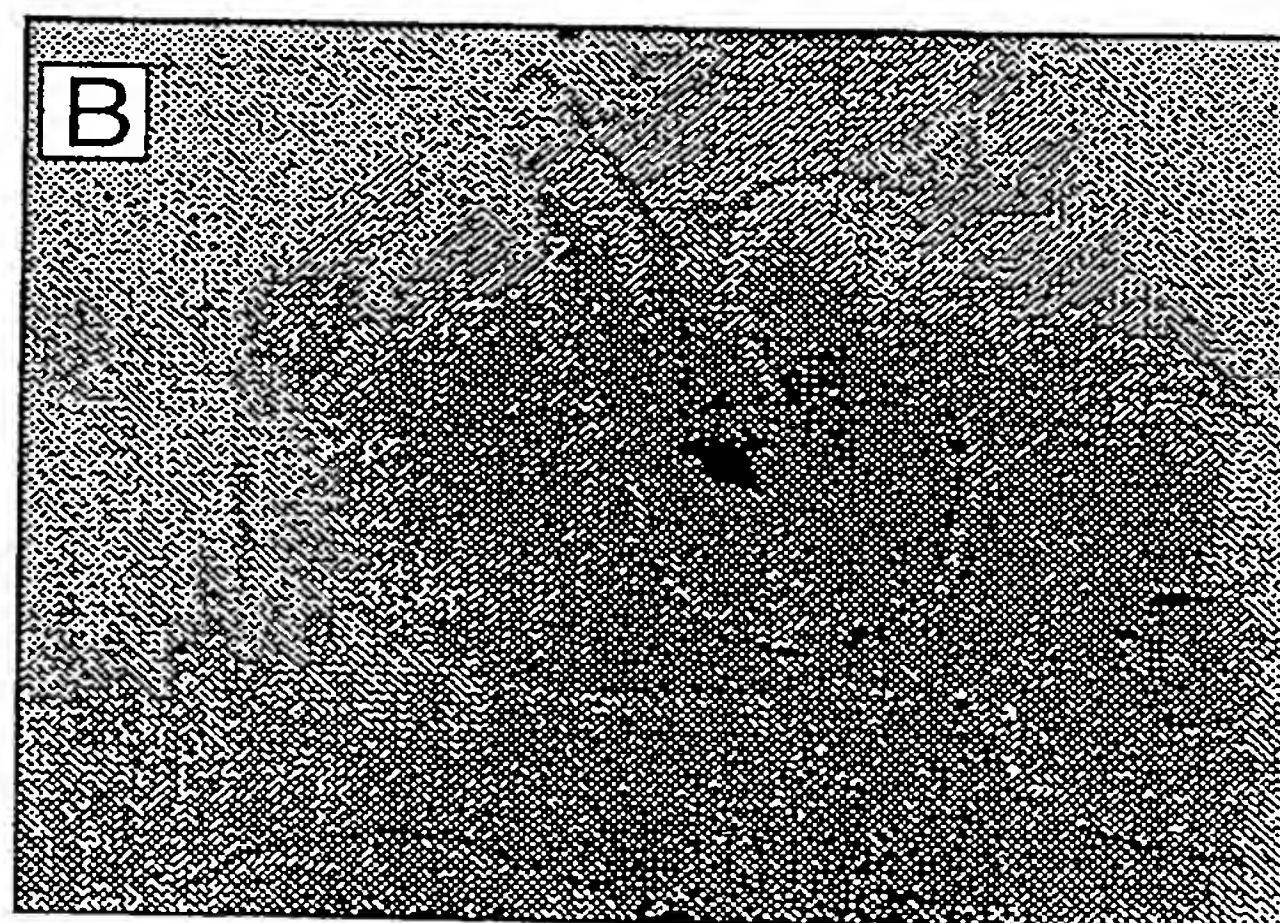
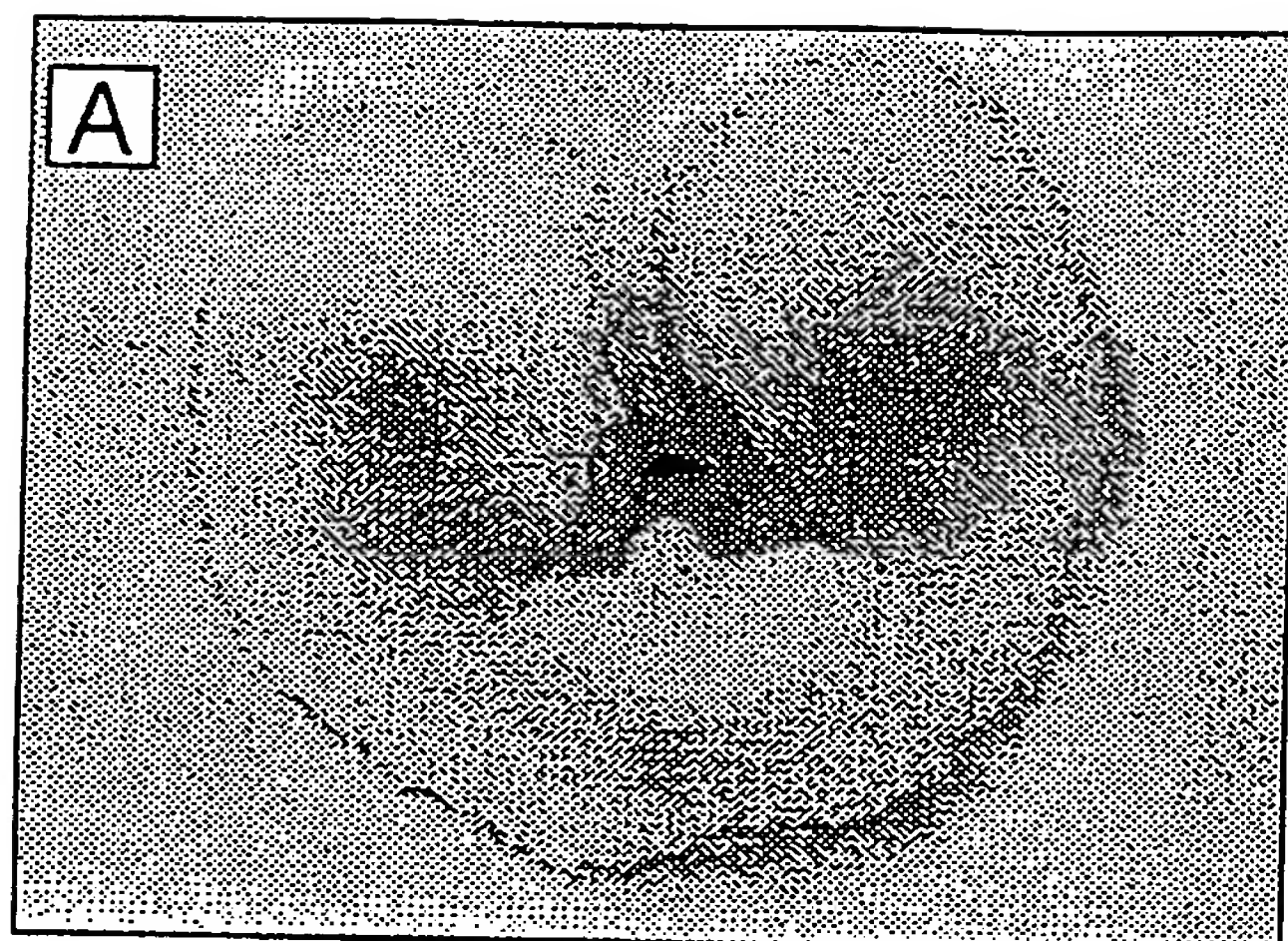
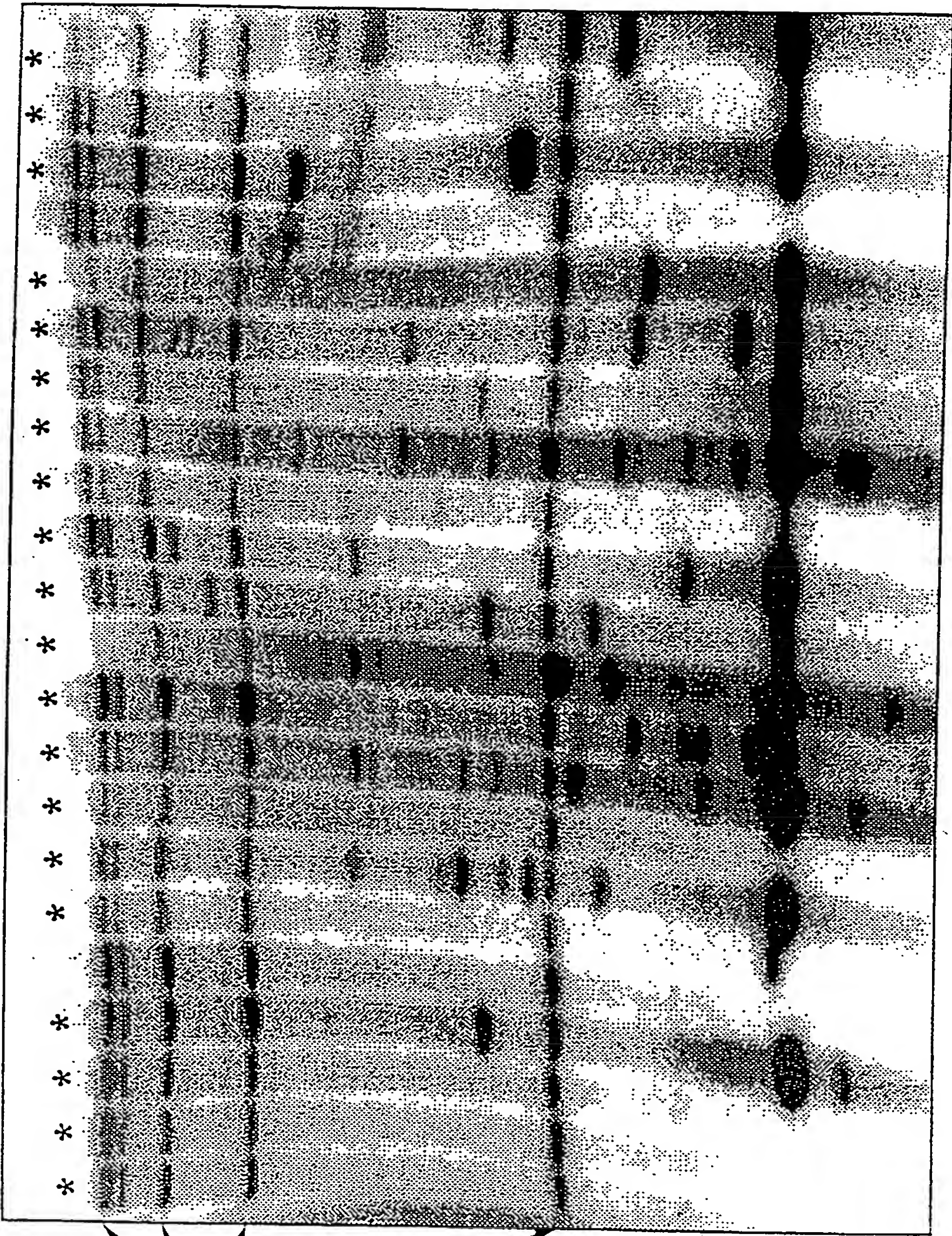


Fig.37.



Endogenous
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1kb SBEII-1
plasmid band

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<120> Improvements in or relating to plant starch composition

<130> C397.01/U

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<150> EP 98307337.0

<151> 1998-09-10

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His Gly Ser Arg Val Lys Val Arg Met Asp Thr Pro Ser Gly Ile Lys
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      50              55              60

Ile Pro Tyr Asn Gly Ile Tyr Tyr Asp Pro Pro Glu Glu Glu Lys Tyr
      65              70              75              80

Val Phe Lys His Pro Gln Pro Lys Arg Pro Lys Ser Leu Arg Ile Tyr
      85              90              95

Glu Thr His Val Gly Met Ser Ser Pro Glu Pro Lys Ile Asn Thr Tyr
      100              105              110

Ala Asn Phe Arg Asp Glu Val Leu Pro Arg Ile Lys Arg Leu Gly Tyr
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Asn Ala Val Gln Ile Met Ala Ile Gln Glu His Ser Tyr Tyr Gly Ser
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 180 185 190
 Leu Asp Gly Leu Asn Gly Phe Asp Gly Thr Asp Thr His Tyr Phe His
 195 200 205
 Gly Gly Ser Arg Gly His His Trp Met Trp Asp Ser Arg Val Phe Asn
 210 215 220
 Tyr Gly Asn Lys Glu Val Ile Arg Phe Leu Leu Ser Asn Ala Arg Trp
 225 230 235 240
 Trp Leu Glu Glu Tyr Lys Phe Asp Gly Phe Arg Phe Asp Gly Ala Thr
 245 250 255
 Ser Met Met Tyr Thr His His Gly Leu Gln Val Thr Phe Thr Gly Ser
 260 265 270
 Tyr His Glu Tyr Phe Gly Phe Ala Thr Asp Val Asp Ala Val Val Tyr
 275 280 285
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 290 295 300
 Thr Ile Gly Glu Asp Val Ser Gly Met Pro Thr Phe Ala Leu Pro Val
 305 310 315 320
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 340 345 350
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 355 360 365
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 Ser Tyr Asp Lys Cys Arg Arg Arg Phe Asp Gln Gly Asp Ala Glu Phe
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 Leu Arg Tyr His Gly Met Gln Gln Phe Asp Gln Ala Met Gln His Leu
 485 490 495
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 Lys His Glu Glu Asp Lys Val Ile Val Phe Glu Lys Gly Asp Leu Val
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 Gly Gly Glu Gly Tyr Leu Asn Phe Met Gly Asn Glu Phe Gly His Pro
 35 40 45
 Glu Trp Ile Asp Phe Pro Arg Gly Pro Gln Val Leu Pro Ser Gly Lys
 50 55 60
 Phe Ile Pro Gly Asn Ser Asn Ser Tyr Asp Lys Cys Arg Arg Arg Phe
 65 70 75 80

Asp Leu Gly Asp Ala Glu Phe Leu Arg Tyr His Gly Met Gln Gln Phe
 85 90 95
 Asp Gln Ala Met Gln His Leu Glu Glu Lys Tyr Gly Phe Met Thr Ser
 100 105 110
 Asp His Gln Tyr Val Ser Arg Lys His Glu Glu Asp Lys Val Ile Val
 115 120 125
 Phe Glu Lys Gly Asp Leu Val Phe Val Phe Asn Phe His Trp Ser Asn
 130 135 140
 Ser Tyr Phe Asp Tyr Arg Val Gly Cys Leu Lys Pro Gly Lys Tyr Lys
 145 150 155 160
 Val Val Leu Asp Ser Asp Ala Gly Leu Phe Gly Gly Phe Gly Arg Ile
 165 170 175
 His His Thr Ala Glu His Phe Thr Ser Asp Cys Gln His Asp Asn Arg
 180 185 190
 Pro His Ser Phe Ser Val Tyr Thr Pro Ser Arg Thr Cys Val Val Tyr
 195 200 205
 Ala Pro Met Asn
 210

<210> 8
 <211> 378
 <212> DNA
 <213> Triticum aestivum

<400> 8
 actaacagca aggtgcagca tacgcgtgcg cgctgttggt gctagtagca agaaaaatcg 60
 tacgggtcaat acagccaggt gcaagggttta ataaggattt tttgcttcaa cgagtcctgg 120
 atagacaaga caacatgatg ttgtggcggtg tgctcccaat cccagggcg ttgtgaagaa 180
 aacatgctca tctgtgttat gattttatgg atcagcgacg aaacttcccc caaatacca 240
 tgcctcctta aatctttgtg gccgtaaacc attgctagtg tcctctaaat tgacagttta 300
 gcatagaggt tttacttttg tatcttcttt ttgacagtta gactttattc ctcaaataat 360
 cgaccagtcg tttactcg 378

<210> 9
 <211> 449
 <212> DNA
 <213> Triticum aestivum

<400> 9

aactaacagc aaagtgcagc atacgcgtgc gcgctgttgt tgctagtagc aagaaaaatc 60
gtatgggtcaa tacaaccagg tgcaagggtt aataaggatt ttgcttcaa cgagtcctgg 120
atagacaaga caacatgatg ttgtgctgtg tgctcccaat cccagggng ttgtgaagaa 180
aacatgctca tctgtgttat tttatggatc agggangaaa cctcccccaa anacccttt 240
tttttttgaa agnggatag gccccggtn tctgcatntg gatgcctcc taaatntttg 300
tagccataaa ccattgctag tgcctntaa attgacagtt tagaatagng gttntacttt 360
tgtattttnt ttttgacagt tagactgtat tcctcaaata atcgacatgt tgtttactcg 420
aagntgagaa ataaaatcag agattgnag 449

<210> 10

<211> 428

<212> DNA

<213> Triticum aestivum

<400> 10

actaaacagc aaagtgcagc atacgcgtgc acgctgttgt tgctagcact agcaagaaaa 60
aatcgtatgg tcaatacaac cagggtgcaag gtttaataag ggtttttgct tcaacgagtc 120
ctggatagac aagacaacat gatgatgtgc tctgtgctcc caaattccca gggcgttgng 180
nggaaaacat gctcatctgt gttatcattt tatggatcag ngnggaaacc tcccccaa 240
acccatgcct ccttaaactt ttgtggctcc aaaccatggc tactatcctc taaattggca 300
gttttagcata gaggttttac ttttgtaaata tttttttgac agttaataga ctctattcct 360
caaataattg acatgtcctt tacaagaaga tgagaaataa aatcagggat tgaagaatcc 420
caaaagct 428

<210> 11

<211> 592

<212> PRT

<213> Triticum aestivum

<400> 11

Phe	Gly	Val	Trp	Glu	Met	Phe	Leu	Pro	Asn	Asn	Ala	Asp	Gly	Ser	Pro
1					5				10					15	
Pro	Ile	Pro	His	Gly	Ser	Arg	Val	Lys	Val	Arg	Met	Asp	Thr	Pro	Ser
			20					25						30	
Gly	Ile	Lys	Asp	Ser	Ile	Pro	Ala	Trp	Ile	Lys	Tyr	Ser	Val	Gln	Thr
		35					40					45			
Pro	Gly	Asp	Ile	Pro	Tyr	Asn	Gly	Ile	Tyr	Tyr	Asp	Pro	Pro	Glu	Glu
	50					55					60				
Glu	Lys	Tyr	Val	Phe	Lys	His	Pro	Gln	Pro	Lys	Arg	Pro	Lys	Ser	Leu
65					70					75				80	
Arg	Ile	Tyr	Glu	Thr	His	Val	Gly	Met	Ser	Ser	Pro	Glu	Pro	Lys	Ile
			85					90						95	

Asn Thr Tyr Ala Asn Phe Arg Asp Glu Val Leu Pro Arg Ile Lys Arg
 100 105 110

Leu Gly Tyr Asn Ala Val Gln Ile Met Ala Ile Gln Glu His Ser Tyr
 115 120 125

Tyr Gly Ser Phe Gly Tyr His Val Thr Asn Phe Phe Ala Pro Ser Ser
 130 135 140

Arg Phe Gly Ser Pro Glu Asp Leu Lys Ser Leu Ile Asp Arg Ala His
 145 150 155 160

Glu Leu Gly Leu Val Val Leu Met Asp Val Val His Ser His Ala Ser
 165 170 175

Asn Asn Thr Leu Asp Gly Leu Asn Gly Phe Asp Gly Thr Asp Thr His
 180 185 190

Tyr Phe His Gly Gly Ser Arg Gly His His Trp Met Trp Asp Ser Arg
 195 200 205

Val Phe Asn Tyr Gly Asn Lys Glu Val Ile Arg Phe Leu Leu Ser Asn
 210 215 220

Ala Arg Trp Trp Leu Glu Glu Tyr Lys Phe Asp Gly Phe Arg Phe Asp
 225 230 235 240

Gly Ala Thr Ser Met Met Tyr Thr His His Gly Leu Gln Val Thr Phe
 245 250 255

Thr Gly Ser Tyr His Glu Tyr Phe Gly Phe Ala Thr Asp Val Asp Ala
 260 265 270

Val Val Tyr Leu Met Leu Met Asn Asp Leu Ile His Gly Phe Tyr Pro
 275 280 285

Glu Ala Val Thr Ile Gly Glu Asp Val Ser Gly Met Pro Thr Phe Ala
 290 295 300

Leu Pro Val Gln Val Gly Gly Val Gly Phe Asp Tyr Arg Leu His Met
 305 310 315 320

Ala Val Ala Asp Lys Trp Ile Glu Leu Leu Lys Gly Asn Asp Glu Ala
 325 330 335

Trp Glu Met Gly Asn Ile Val His Thr Leu Thr Asn Arg Arg Trp Pro
 340 345 350

Glu Lys Cys Val Thr Tyr Ala Glu Ser His Asp Gln Ala Leu Val Gly
 355 360 365

Asp Lys Thr Ile Ala Phe Trp Leu Met Asp Lys Asp Met Tyr Asp Phe
 370 375 380

Met Ala Leu Asn Gly Pro Ser Thr Pro Ser Ile Asp Arg Gly Ile Ala
 385 390 395 400

Leu His Lys Met Ile Arg Leu Ile Thr Met Gly Leu Gly Gly Glu Gly
 405 410 415

Tyr Leu Asn Phe Met Gly Asn Glu Phe Gly His Pro Glu Trp Ile Asp
 420 425 430

Phe Pro Arg Gly Pro Gln Val Leu Pro Thr Gly Lys Phe Ile Pro Gly
 435 440 445

Asn Asn Asn Ser Tyr Asp Lys Cys Arg Arg Arg Phe Asp Gln Gly Asp
 450 455 460

Ala Glu Phe Leu Arg Tyr His Gly Met Gln Gln Phe Asp Gln Ala Met
 465 470 475 480

Gln His Leu Glu Glu Lys Tyr Gly Phe Met Thr Ser Asp His Gln Tyr
 485 490 495

Val Ser Arg Lys His Glu Glu Asp Lys Val Ile Val Phe Glu Lys Gly
 500 505 510

Asp Leu Val Phe Val Phe Asn Phe His Trp Ser Asn Ser Tyr Phe Asp
 515 520 525

Tyr Arg Val Gly Cys Leu Lys Pro Gly Lys Tyr Lys Val Val Leu Asp
 530 535 540

Ser Asp Ala Gly Leu Phe Gly Gly Phe Gly Arg Ile His His Thr Ala
 545 550 555 560

Glu His Phe Thr Ser Asp Cys Gln His Asp Asn Arg Pro His Ser Phe
 565 570 575

Ser Val Tyr Thr Pro Ser Arg Thr Cys Val Val Tyr Ala Pro Met Asn
 580 585 590

<210> 12

<211> 771

<212> PRT

<213> Triticum aestivum

<400> 12

Ser Arg Ala Ala Ser Pro Gly Lys Val Leu Val Pro Asp Gly Glu Ser
 1 5 10 15

Asp Asp Leu Ala Ser Pro Ala Gln Pro Glu Glu Leu Gln Ile Pro Glu
 20 25 30

Asp Ile Glu Glu Gln Thr Ala Glu Val Asn Met Thr Gly Gly Thr Ala
 35 40 45

Glu Lys Leu Glu Ser Ser Glu Pro Thr Gln Gly Ile Val Glu Thr Ile
 50 55 60

Thr Asp Gly Val Thr Lys Gly Val Lys Glu Leu Val Val Gly Glu Lys
 65 70 75 80

Pro Arg Val Val Pro Lys Pro Gly Asp Gly Gln Lys Ile Tyr Glu Ile
 85 90 95

Asp Pro Thr Leu Lys Asp Phe Arg Ser His Leu Asp Tyr Arg Tyr Ser
 100 105 110

Glu Tyr Arg Arg Ile Arg Ala Ala Ile Asp Gln His Glu Gly Gly Leu
 115 120 125

Glu Ala Phe Ser Arg Gly Tyr Glu Lys Leu Gly Phe Thr Arg Ser Ala
 130 135 140

Glu Gly Ile Thr Tyr Arg Glu Trp Ala Pro Gly Ala His Ser Ala Ala
 145 150 155 160

Leu Val Gly Asp Phe Asn Asn Trp Asn Pro Asn Ala Asp Thr Met Thr
 165 170 175

Arg Asp Asp Tyr Gly Val Trp Glu Ile Phe Leu Pro Asn Asn Ala Asp
 180 185 190

Gly Ser Pro Ala Ile Pro His Gly Ser Arg Val Lys Ile Arg Met Asp
 195 200 205

Thr Pro Ser Gly Val Lys Asp Ser Ile Ser Ala Trp Ile Lys Phe Ser

210	215	220
Val Gln Ala Pro Gly Glu Ile Pro Phe Asn Gly Ile Tyr Tyr Asp Pro		
225	230	235 240
Pro Glu Glu Glu Lys Tyr Val Phe Gln His Pro Gln Pro Lys Arg Pro		
245	250	255
Glu Ser Leu Arg Ile Tyr Glu Ser His Ile Gly Met Ser Ser Pro Glu		
260	265	270
Pro Lys Ile Asn Ser Tyr Ala Asn Phe Arg Asp Glu Val Leu Pro Arg		
275	280	285
Ile Lys Arg Leu Gly Tyr Asn Ala Val Gln Ile Met Ala Ile Gln Glu		
290	295	300
His Ser Tyr Tyr Ala Ser Phe Gly Tyr His Val Thr Asn Phe Phe Ala		
305	310	315 320
Pro Ser Ser Arg Phe Gly Thr Pro Glu Asp Leu Lys Ser Leu Ile Asp		
325	330	335
Arg Ala His Glu Leu Gly Leu Ile Val Leu Met Asp Ile Val His Ser		
340	345	350
His Ser Ser Asn Asn Thr Leu Asp Gly Leu Asn Gly Phe Asp Gly Thr		
355	360	365
Asp Thr His Tyr Phe His Gly Gly Pro Arg Gly His His Trp Met Trp		
370	375	380
Asp Ser Arg Leu Phe Asn Tyr Gly Ser Trp Glu Val Leu Arg Phe Leu		
385	390	395 400
Leu Ser Asn Ala Arg Trp Trp Leu Glu Glu Tyr Lys Phe Asp Gly Phe		
405	410	415
Arg Phe Asp Gly Val Thr Ser Met Met Tyr Thr His His Gly Leu Gln		
420	425	430
Met Thr Phe Thr Gly Asn Tyr Gly Glu Tyr Phe Gly Phe Ala Thr Asp		
435	440	445
Val Asp Ala Val Val Tyr Leu Met Leu Val Asn Asp Leu Ile His Gly		
450	455	460
Leu His Pro Asp Ala Val Ser Ile Gly Glu Asp Val Ser Gly Met Pro		

465		470		475		480
Thr Phe Cys Ile Pro Val Pro Asp Gly Gly Val Gly Leu Asp Tyr Arg						
	485		490		495	
Leu His Met Ala Val Ala Asp Lys Trp Ile Glu Leu Leu Lys Gln Ser						
	500		505		510	
Asp Glu Ser Trp Lys Met Gly Asp Ile Val His Thr Leu Thr Asn Arg						
	515		520		525	
Arg Trp Leu Glu Lys Cys Val Thr Tyr Ala Glu Ser His Asp Gln Ala						
	530		535		540	
Leu Val Gly Asp Lys Thr Ile Ala Phe Trp Leu Met Asp Lys Asp Met						
	545		550		555	560
Tyr Asp Phe Met Ala Leu Asp Arg Pro Ser Thr Pro Arg Ile Asp Arg						
	565		570		575	
Gly Ile Ala Leu His Lys Met Ile Arg Leu Val Thr Met Gly Leu Gly						
	580		585		590	
Gly Glu Gly Tyr Leu Asn Phe Met Gly Asn Glu Phe Gly His Pro Glu						
	595		600		605	
Trp Ile Asp Phe Pro Arg Gly Pro Gln Thr Leu Pro Thr Gly Lys Val						
	610		615		620	
Leu Pro Gly Asn Asn Asn Ser Tyr Asp Lys Cys Arg Arg Arg Phe Asp						
	625		630		635	640
Leu Gly Asp Ala Asp Phe Leu Arg Tyr His Gly Met Gln Glu Phe Asp						
	645		650		655	
Gln Ala Met Gln His Leu Glu Glu Lys Tyr Gly Phe Met Thr Ser Glu						
	660		665		670	
His Gln Tyr Val Ser Arg Lys His Glu Glu Asp Lys Val Ile Ile Phe						
	675		680		685	
Glu Arg Gly Asp Leu Val Phe Val Phe Asn Phe His Trp Ser Asn Ser						
	690		695		700	
Phe Phe Asp Tyr Arg Val Gly Cys Ser Arg Pro Gly Lys Tyr Lys Val						
	705		710		715	720
Ala Leu Asp Ser Asp Asp Ala Leu Phe Gly Gly Phe Ser Arg Leu Asp						

725

730

735

His Asp Val Asp Tyr Phe Thr Thr Glu His Pro His Asp Asn Arg Pro
 740 745 750

Arg Ser Phe Ser Val Tyr Thr Pro Ser Arg Thr Ala Val Val Tyr Ala
 755 760 765

Leu Thr Glu
 770

<210> 13

<211> 797

<212> PRT

<213> Zea mays

<400> 13

Ser Cys Ala Gly Ala Pro Gly Lys Val Leu Val Pro Gly Gly Gly Ser
 1 5 10 15

Asp Asp Leu Leu Ser Ser Ala Glu Pro Val Val Asp Thr Gln Pro Glu
 20 25 30

Glu Leu Gln Ile Pro Glu Ala Glu Leu Thr Val Glu Lys Thr Ser Ser
 35 40 45

Ser Pro Thr Gln Thr Thr Ser Ala Val Ala Glu Ala Ser Ser Gly Val
 50 55 60

Glu Ala Glu Glu Arg Pro Glu Leu Ser Ser Glu Val Ile Gly Val Gly
 65 70 75 80

Gly Thr Gly Gly Thr Lys Ile Asp Gly Ala Gly Ile Lys Ala Lys Ala
 85 90 95

Pro Leu Val Glu Glu Lys Pro Arg Val Ile Pro Pro Pro Gly Asp Gly
 100 105 110

Gln Arg Ile Tyr Glu Ile Asp Pro Met Leu Glu Gly Phe Arg Gly His
 115 120 125

Leu Asp Tyr Arg Tyr Ser Glu Tyr Lys Arg Leu Arg Ala Ala Ile Asp
 130 135 140

Gln His Glu Gly Gly Leu Asp Ala Phe Ser Arg Gly Tyr Glu Lys Leu
 145 150 155 160

Gly Phe Thr Arg Ser Ala Glu Gly Ile Thr Tyr Arg Glu Trp Ala Pro
 165 170 175

Gly Ala Tyr Ser Ala Ala Leu Val Gly Asp Phe Asn Asn Trp Asn Pro
 180 185 190

Asn Ala Asp Ala Met Ala Arg Asn Glu Tyr Gly Val Trp Glu Ile Phe
 195 200 205

Leu Pro Asn Asn Ala Asp Gly Ser Pro Ala Ile Pro His Gly Ser Arg
 210 215 220

Val Lys Ile Arg Met Asp Thr Pro Ser Gly Val Lys Asp Ser Ile Pro
 225 230 235 240

Ala Trp Ile Lys Phe Ser Val Gln Ala Pro Gly Glu Ile Pro Tyr Asn
 245 250 255

Gly Ile Tyr Tyr Asp Pro Pro Glu Glu Glu Lys Tyr Val Phe Lys His
 260 265 270

Pro Gln Pro Lys Arg Pro Lys Ser Leu Arg Ile Tyr Glu Ser His Val
 275 280 285

Gly Met Ser Ser Pro Glu Pro Lys Ile Asn Thr Tyr Ala Asn Phe Arg
 290 295 300

Asp Glu Val Leu Pro Arg Ile Lys Lys Leu Gly Tyr Asn Ala Val Gln
 305 310 315 320

Ile Met Ala Ile Gln Glu His Ser Tyr Tyr Ala Ser Phe Gly Tyr His
 325 330 335

Val Thr Asn Phe Phe Ala Pro Ser Ser Arg Phe Gly Thr Pro Glu Asp
 340 345 350

Leu Lys Ser Leu Ile Asp Lys Ala His Glu Leu Gly Leu Leu Val Leu
 355 360 365

Met Asp Ile Val His Ser His Ser Ser Asn Asn Thr Leu Asp Gly Leu
 370 375 380

Asn Gly Phe Asp Gly Thr Asp Thr His Tyr Phe His Gly Gly Pro Arg
 385 390 395 400

Gly His His Trp Met Trp Asp Ser Arg Leu Phe Asn Tyr Gly Ser Trp
 405 410 415

Glu Val Leu Arg Phe Leu Leu Ser Asn Ala Arg Trp Trp Leu Glu Glu
 420 425 430
 Tyr Lys Phe Asp Gly Phe Arg Phe Asp Gly Val Thr Ser Met Met Tyr
 435 440 445
 Thr His His Gly Leu Gln Val Thr Phe Thr Gly Asn Tyr Gly Glu Tyr
 450 455 460
 Phe Gly Phe Ala Thr Asp Val Asp Ala Val Val Tyr Leu Met Leu Val
 465 470 475 480
 Asn Asp Leu Ile Arg Gly Leu Tyr Pro Glu Ala Val Ser Ile Gly Glu
 485 490 495
 Asp Val Ser Gly Met Pro Thr Phe Cys Ile Pro Val Gln Asp Gly Gly
 500 505 510
 Val Gly Phe Asp Tyr Arg Leu His Met Ala Val Pro Asp Lys Trp Ile
 515 520 525
 Glu Leu Leu Lys Gln Ser Asp Glu Tyr Trp Glu Met Gly Asp Ile Val
 530 535 540
 His Thr Leu Thr Asn Arg Arg Trp Leu Glu Lys Cys Val Thr Tyr Cys
 545 550 555 560
 Glu Ser His Asp Gln Ala Leu Val Gly Asp Lys Thr Ile Ala Phe Trp
 565 570 575
 Leu Met Asp Lys Asp Met Tyr Asp Phe Met Ala Leu Asp Arg Pro Ser
 580 585 590
 Thr Pro Arg Ile Asp Arg Gly Ile Ala Leu His Lys Met Ile Arg Leu
 595 600 605
 Val Thr Met Gly Leu Gly Gly Glu Gly Tyr Leu Asn Phe Met Gly Asn
 610 615 620
 Glu Phe Gly His Pro Glu Trp Ile Asp Phe Pro Arg Gly Pro Gln Ser
 625 630 635 640
 Leu Pro Asn Gly Ser Val Ile Pro Gly Asn Asn Asn Ser Phe Asp Lys
 645 650 655
 Cys Arg Arg Arg Phe Asp Leu Gly Asp Ala Asp Tyr Leu Arg Tyr Arg
 660 665 670

18

Gly Met Gln Glu Phe Asp Gln Ala Met Gln His Leu Glu Gly Lys Tyr
 675 680 685

Glu Phe Met Thr Ser Asp His Ser Tyr Val Ser Arg Lys His Glu Glu
 690 695 700

Asp Lys Val Ile Ile Phe Glu Arg Gly Asp Leu Val Phe Val Phe Asn
 705 710 715 720

Phe His Trp Ser Asn Ser Tyr Phe Asp Tyr Arg Val Gly Cys Phe Lys
 725 730 735

Pro Gly Lys Tyr Lys Ile Val Leu Asp Ser Asp Asp Gly Leu Phe Gly
 740 745 750

Gly Phe Ser Arg Leu Asp His Asp Ala Glu Tyr Phe Thr Ala Asp Trp
 755 760 765

Pro His Asp Asn Arg Pro Cys Ser Phe Ser Val Tyr Ala Pro Ser Arg
 770 775 780

Thr Ala Val Val Tyr Ala Pro Ala Gly Ala Glu Asp Glu
 785 790 795

<210> 14

<211> 747

<212> PRT

<213> Zea mays

<400> 14

Ala Ala Ala Ala Ala Arg Lys Ala Val Met Val Pro Glu Gly Glu Asn
 1 5 10 15

Asp Gly Leu Ala Ser Arg Ala Asp Ser Ala Gln Phe Gln Ser Asp Glu
 20 25 30

Leu Glu Val Pro Asp Ile Ser Glu Glu Thr Thr Cys Gly Ala Gly Val
 35 40 45

Ala Asp Ala Gln Ala Leu Asn Arg Val Arg Val Val Pro Pro Pro Ser
 50 55 60

Asp Gly Gln Lys Ile Phe Gln Ile Asp Pro Met Leu Gln Gly Tyr Lys
 65 70 75 80

Tyr His Leu Glu Tyr Arg Tyr Ser Leu Tyr Arg Arg Ile Arg Ser Asp
 85 90 95

Ile Asp Glu His Glu Gly Gly Leu Glu Ala Phe Ser Arg Ser Tyr Glu
 100 105 110
 Lys Phe Gly Phe Asn Ala Ser Ala Glu Gly Ile Thr Tyr Arg Glu Trp
 115 120 125
 Ala Pro Gly Ala Phe Ser Ala Ala Leu Val Gly Asp Val Asn Asn Trp
 130 135 140
 Asp Pro Asn Ala Asp Arg Met Ser Lys Asn Glu Phe Gly Val Trp Glu
 145 150 155 160
 Ile Phe Leu Pro Asn Asn Ala Asp Gly Thr Ser Pro Ile Pro His Gly
 165 170 175
 Ser Arg Val Lys Val Arg Met Asp Thr Pro Ser Gly Ile Lys Asp Ser
 180 185 190
 Ile Pro Ala Trp Ile Lys Tyr Ser Val Gln Ala Pro Gly Glu Ile Pro
 195 200 205
 Tyr Asp Gly Ile Tyr Tyr Asp Pro Pro Glu Glu Val Lys Tyr Val Phe
 210 215 220
 Arg His Ala Gln Pro Lys Arg Pro Lys Ser Leu Arg Ile Tyr Glu Thr
 225 230 235 240
 His Val Gly Met Ser Ser Pro Glu Pro Lys Ile Asn Thr Tyr Val Asn
 245 250 255
 Phe Arg Asp Glu Val Leu Pro Arg Ile Lys Lys Leu Gly Tyr Asn Ala
 260 265 270
 Val Gln Ile Met Ala Ile Gln Glu His Ser Tyr Tyr Gly Ser Phe Gly
 275 280 285
 Tyr His Val Thr Asn Phe Phe Ala Pro Ser Ser Arg Phe Gly Thr Pro
 290 295 300
 Glu Asp Leu Lys Ser Leu Ile Asp Arg Ala His Glu Leu Gly Leu Leu
 305 310 315 320
 Val Leu Met Asp Val Val His Ser His Ala Ser Ser Asn Thr Leu Asp
 325 330 335
 Gly Leu Asn Gly Phe Asp Gly Thr Asp Thr His Tyr Phe His Ser Gly
 340 345 350

Pro Arg Gly His His Trp Met Trp Asp Ser Arg Leu Phe Asn Tyr Gly
 355 360 365

Asn Trp Glu Val Leu Arg Phe Leu Leu Ser Asn Ala Arg Trp Trp Leu
 370 375 380

Glu Glu Tyr Lys Phe Asp Gly Phe Arg Phe Asp Gly Val Thr Ser Met
 385 390 395 400

Met Tyr Thr His His Gly Leu Gln Val Thr Phe Thr Gly Asn Phe Asn
 405 410 415

Glu Tyr Phe Gly Phe Ala Thr Asp Val Asp Ala Val Val Tyr Leu Met
 420 425 430

Leu Val Asn Asp Leu Ile His Gly Leu Tyr Pro Glu Ala Val Thr Ile
 435 440 445

Gly Glu Asp Val Ser Gly Met Pro Thr Phe Ala Leu Pro Val His Asp
 450 455 460

Gly Gly Val Gly Phe Asp Tyr Arg Met His Met Ala Val Ala Asp Lys
 465 470 475 480

Trp Ile Asp Leu Leu Lys Gln Ser Asp Glu Thr Trp Lys Met Gly Asp
 485 490 495

Ile Val His Thr Leu Thr Asn Arg Arg Trp Leu Glu Lys Cys Val Thr
 500 505 510

Tyr Ala Glu Ser His Asp Gln Ala Leu Val Gly Asp Lys Thr Ile Ala
 515 520 525

Phe Trp Leu Met Asp Lys Asp Met Tyr Asp Phe Met Ala Leu Asp Arg
 530 535 540

Pro Ser Thr Pro Thr Ile Asp Arg Gly Ile Ala Leu His Lys Met Ile
 545 550 555 560

Arg Leu Ile Thr Met Gly Leu Gly Gly Glu Gly Tyr Leu Asn Phe Met
 565 570 575

Gly Asn Glu Phe Gly His Pro Glu Trp Ile Asp Phe Pro Arg Gly Pro
 580 585 590

Gln Arg Leu Pro Ser Gly Lys Phe Ile Pro Gly Asn Asn Asn Ser Tyr
 595 600 605

Asp Lys Cys Arg Arg Arg Phe Asp Leu Gly Asp Ala Asp Tyr Leu Arg
 610 615 620

Tyr His Gly Met Gln Glu Phe Asp Gln Ala Met Gln His Leu Glu Gln
 625 630 635 640

Lys Tyr Glu Phe Met Thr Ser Asp His Gln Tyr Ile Ser Arg Lys His
 645 650 655

Glu Glu Asp Lys Val Ile Val Phe Glu Lys Gly Asp Leu Val Phe Val
 660 665 670

Phe Asn Phe His Cys Asn Asn Ser Tyr Phe Asp Tyr Arg Ile Gly Cys
 675 680 685

Arg Lys Pro Gly Val Tyr Lys Val Val Leu Asp Ser Asp Ala Gly Leu
 690 695 700

Phe Gly Gly Phe Ser Arg Ile His His Ala Ala Glu His Phe Thr Ala
 705 710 715 720

Asp Cys Ser His Asp Asn Arg Pro Tyr Ser Phe Ser Val Tyr Thr Pro
 725 730 735

Ser Arg Thr Cys Val Val Tyr Ala Pro Val Glu
 740 745

<210> 15

<211> 50

<212> PRT

<213> Hordeum vulgare

<400> 15

Asn Asp Leu Gly Ile Trp Glu Ile Phe Leu Pro Asn Asn Ala Asp Gly
 1 5 10 15

Ser Pro Pro Ile Pro His Gly Ser Arg Val Lys Val Arg Met Asp Thr
 20 25 30

Pro Ser Gly Thr Lys Asp Ser Ile Pro Ala Trp Ile Lys Phe Ser Val
 35 40 45

Gln Ala
 50

22

<210> 16

<211> 50

<212> PRT

<213> Hordeum vulgare

<400> 16

Asp Asp Tyr Gly Val Trp Glu Ile Phe Leu Pro Asn Asn Ala Asp Gly
 1 5 10 15

Ser Pro Ala Ile Pro His Gly Ser Arg Val Lys Ile Arg Met Asp Thr
 20 25 30

Pro Ser Gly Val Lys Asp Ser Ile Ser Ala Trp Ile Lys Phe Ser Val
 35 40 45

Gln Ala
 50

<210> 17

<211> 760

<212> PRT

<213> Oryza sativa

<400> 17

Ala Ala Gly Ala Ser Gly Glu Val Met Ile Pro Glu Gly Glu Ser Asp
 1 5 10 15

Gly Met Pro Val Ser Ala Gly Ser Asp Asp Leu Gln Leu Pro Ala Leu
 20 25 30

Asp Asp Glu Leu Ser Thr Glu Val Gly Ala Glu Val Glu Ile Glu Ser
 35 40 45

Ser Gly Ala Ser Asp Val Glu Gly Val Lys Arg Val Val Glu Glu Leu
 50 55 60

Ala Ala Glu Gln Lys Pro Arg Val Val Pro Pro Thr Gly Asp Gly Gln
 65 70 75 80

Lys Ile Phe Gln Met Asp Ser Met Leu Asn Gly Tyr Lys Tyr His Leu
 85 90 95

Glu Tyr Arg Tyr Ser Leu Tyr Arg Arg Leu Arg Ser Asp Ile Asp Gln
 100 105 110

Tyr Glu Gly Gly Leu Glu Thr Phe Ser Arg Gly Tyr Glu Lys Phe Gly
 115 120 125

Phe Asn His Ser Ala Glu Gly Val Thr Tyr Arg Glu Trp Ala Pro Gly
 130 135 140

Ala His Ser Ala Ala Leu Val Gly Asp Phe Asn Asn Trp Asn Pro Asn
 145 150 155 160

Ala Asp Arg Met Ser Lys Asn Glu Phe Gly Val Trp Glu Ile Phe Leu
 165 170 175

Pro Asn Asn Ala Asp Gly Ser Ser Pro Ile Pro His Gly Ser Arg Val
 180 185 190

Lys Val Arg Met Glu Thr Pro Ser Gly Ile Lys Asp Ser Ile Pro Ala
 195 200 205

Trp Ile Lys Tyr Ser Val Gln Ala Ala Gly Glu Ile Pro Tyr Asn Gly
 210 215 220

Ile Tyr Tyr Asp Pro Pro Glu Glu Glu Lys Tyr Ile Phe Lys His Pro
 225 230 235 240

Gln Pro Lys Arg Pro Lys Ser Leu Arg Ile Tyr Glu Thr His Val Gly
 245 250 255

Met Ser Ser Thr Glu Pro Lys Ile Asn Thr Tyr Ala Asn Phe Arg Asp
 260 265 270

Glu Val Leu Pro Arg Ile Lys Lys Leu Gly Tyr Asn Ala Val Gln Ile
 275 280 285

Met Ala Ile Gln Glu His Ala Tyr Tyr Gly Ser Phe Gly Tyr His Val
 290 295 300

Thr Asn Phe Phe Ala Pro Ser Ser Arg Phe Gly Thr Pro Glu Asp Leu
 305 310 315 320

Lys Ser Leu Ile Asp Lys Ala His Glu Leu Gly Leu Val Val Leu Met
 325 330 335

Asp Val Val His Ser His Ala Ser Asn Asn Thr Leu Asp Gly Leu Asn
 340 345 350

Gly Phe Asp Gly Thr Asp Thr His Tyr Phe His Ser Gly Ser Arg Gly
 355 360 365

His His Trp Met Trp Asp Ser Arg Leu Phe Asn Tyr Gly Asn Trp Glu
 370 375 380

Val Leu Arg Phe Leu Leu Ser Asn Ala Arg Trp Trp Leu Glu Glu Tyr
 385 390 395 400
 Lys Phe Asp Gly Phe Arg Phe Asp Gly Val Thr Ser Met Met Tyr Thr
 405 410 415
 His His Gly Leu Gln Val Ala Phe Thr Gly Asn Tyr Ser Glu Tyr Phe
 420 425 430
 Gly Phe Ala Thr Asp Ala Asp Ala Val Val Tyr Leu Met Leu Val Asn
 435 440 445
 Asp Leu Ile His Gly Leu Tyr Pro Glu Ala Ile Thr Ile Gly Glu Asp
 450 455 460
 Val Ser Gly Met Pro Thr Phe Ala Leu Pro Val Gln Asp Gly Gly Val
 465 470 475 480
 Gly Phe Asp Tyr Arg Leu His Met Ala Val Pro Asp Lys Trp Ile Glu
 485 490 495
 Leu Leu Lys Gln Ser Asp Glu Ser Trp Lys Met Gly Asp Ile Val His
 500 505 510
 Thr Leu Thr Asn Arg Arg Trp Ser Glu Lys Cys Val Thr Tyr Ala Glu
 515 520 525
 Ser His Asp Gln Ala Leu Val Gly Asp Lys Thr Ile Ala Phe Trp Leu
 530 535 540
 Met Asp Lys Asp Met Tyr Asp Phe Met Ala Leu Asp Arg Pro Ala Thr
 545 550 555 560
 Pro Ser Ile Asp Arg Gly Ile Ala Leu His Lys Met Ile Arg Leu Ile
 565 570 575
 Thr Met Gly Leu Gly Gly Glu Gly Tyr Leu Asn Phe Met Gly Asn Glu
 580 585 590
 Phe Gly His Pro Glu Trp Ile Asp Phe Pro Arg Ala Pro Gln Val Leu
 595 600 605
 Pro Asn Gly Lys Phe Ile Pro Gly Asn Asn Asn Ser Tyr Asp Lys Cys
 610 615 620
 Arg Arg Arg Phe Asp Leu Gly Asp Ala Asp Tyr Leu Arg Tyr Arg Gly
 625 630 635 640

Met Leu Glu Phe Asp Arg Ala Met Gln Ser Leu Glu Glu Lys Tyr Gly
 645 650 655

Phe Met Thr Ser Asp His Gln Tyr Ile Ser Arg Lys His Glu Glu Asp
 660 665 670

Lys Met Ile Ile Phe Glu Lys Gly Asp Leu Val Phe Val Phe Asn Phe
 675 680 685

His Trp Ser Asn Ser Tyr Phe Asp Tyr Arg Val Gly Cys Leu Lys Pro
 690 695 700

Gly Lys Tyr Lys Val Val Leu Asp Ser Asp Ala Gly Leu Phe Gly Gly
 705 710 715 720

Phe Gly Arg Ile His His Thr Ala Glu His Phe Thr Ala Asp Cys Ser
 725 730 735

His Asp Asn Arg Pro Tyr Ser Phe Ser Val Tyr Ser Pro Ser Arg Thr
 740 745 750

Cys Val Val Tyr Ala Pro Ala Glu
 755 760

<210> 18

<211> 844

<212> PRT

<213> Oryza sativa

<400> 18

Val Glu Ala Glu Arg Gly Gly Cys Arg Gly Ile Arg Ser Gly Cys Gly
 1 5 10 15

Ala Gly Glu Met Ala Ala Pro Ala Ser Ala Val Pro Gly Ser Ala Ala
 20 25 30

Gly Leu Arg Ala Gly Ala Val Arg Phe Pro Val Pro Ala Gly Ala Arg
 35 40 45

Ser Trp Arg Ala Ala Ala Glu Leu Pro Thr Ser Arg Ser Leu Leu Ser
 50 55 60

Gly Arg Arg Phe Pro Gly Ala Val Arg Val Gly Gly Ser Gly Gly Arg
 65 70 75 80

Val Ala Val Arg Ala Ala Gly Ala Ser Gly Glu Val Met Ile Pro Glu

PCT/GB99/03011

SUBSTITUTE SHEET (RULE 26)

27
 340 345 350
 Asn Phe Arg Asp Glu Val Leu Pro Arg Ile Lys Lys Leu Gly Tyr Asn
 355 360 365
 Ala Val Gln Ile Met Ala Ile Gln Glu His Ala Tyr Tyr Gly Ser Phe
 370 375 380
 Gly Tyr His Val Thr Asn Phe Phe Ala Pro Ser Ser Arg Phe Gly Thr
 385 390 395 400
 Pro Glu Asp Leu Lys Ser Leu Ile Asp Lys Ala His Glu Leu Gly Leu
 405 410 415
 Val Val Leu Met Asp Val Val His Ser His Ala Ser Asn Asn Thr Leu
 420 425 430
 Asp Gly Leu Asn Gly Phe Asp Gly Thr Asp Thr His Tyr Phe His Ser
 435 440 445
 Gly Ser Arg Gly His His Trp Met Trp Asp Ser Arg Leu Phe Asn Tyr
 450 455 460
 Gly Asn Trp Glu Val Leu Arg Phe Leu Leu Ser Asn Ala Arg Trp Trp
 465 470 475 480
 Leu Glu Glu Tyr Lys Phe Asp Gly Phe Arg Phe Asp Gly Val Thr Ser
 485 490 495
 Met Met Tyr Thr His His Gly Leu Gln Val Ala Phe Thr Gly Asn Tyr
 500 505 510
 Ser Glu Tyr Phe Gly Phe Ala Thr Asp Ala Asp Ala Val Val Tyr Leu
 515 520 525
 Met Leu Val Asn Asp Leu Ile His Gly Leu Tyr Pro Glu Ala Ile Thr
 530 535 540
 Ile Gly Glu Asp Val Ser Gly Met Pro Thr Phe Ala Leu Pro Val Gln
 545 550 555 560
 Asp Gly Gly Val Gly Phe Asp Tyr Arg Leu His Met Ala Val Pro Asp
 565 570 575
 Lys Trp Ile Glu Leu Leu Lys Gln Ser Asp Glu Ser Trp Lys Met Gly
 580 585 590
 Asp Ile Val His Thr Leu Thr Asn Arg Arg Trp Ser Glu Lys Cys Val

595	600	605
Thr Tyr Ala Glu Ser His Asp Gln Ala Leu Val Gly Asp Lys Thr Ile		
610	615	620
Ala Phe Trp Leu Met Asp Lys Asp Met Tyr Asp Phe Met Ala Leu Asp		
625	630	635 640
Arg Pro Ala Thr Pro Ser Ile Asp Arg Gly Ile Ala Leu His Lys Met		
	645	650 655
Ile Arg Leu Ile Thr Met Gly Leu Gly Gly Glu Gly Tyr Leu Asn Phe		
	660	665 670
Met Gly Asn Glu Phe Gly His Pro Glu Trp Ile Asp Phe Pro Arg Ala		
	675	680 685
Pro Gln Val Leu Pro Asn Gly Lys Phe Ile Pro Gly Asn Asn Asn Ser		
	690	695 700
Tyr Asp Lys Cys Arg Arg Arg Phe Asp Leu Gly Asp Ala Asp Tyr Leu		
705	710	715 720
Arg Tyr Arg Gly Met Leu Glu Phe Asp Arg Ala Met Gln Ser Leu Glu		
	725	730 735
Glu Lys Tyr Gly Phe Met Thr Ser Asp His Gln Tyr Ile Ser Arg Lys		
	740	745 750
His Glu Glu Asp Lys Met Ile Ile Phe Glu Lys Gly Asp Leu Val Phe		
	755	760 765
Val Phe Asn Phe His Trp Ser Asn Ser Tyr Phe Asp Tyr Arg Val Gly		
	770	775 780
Cys Leu Lys Pro Gly Lys Tyr Lys Val Val Leu Asp Ser Asp Ala Gly		
785	790	795 800
Leu Phe Gly Gly Phe Gly Arg Ile His His Thr Ala Glu His Phe Thr		
	805	810 815
Ala Asp Cys Ser His Asp Asn Arg Pro Tyr Ser Phe Ser Val Tyr Ser		
	820	825 830
Pro Ser Arg Thr Cys Val Val Tyr Ala Pro Ala Glu		
	835	840

<210> 19
 <211> 857
 <212> PRT
 <213> Pisum sativum

<400> 19

Lys Val Leu Ile Pro Glu Asp Gln Asp Asn Ser Val Ser Leu Ala Asp
 1 5 10 15

Gln Leu Glu Asn Pro Asp Ile Thr Ser Glu Asp Ala Gln Asn Leu Glu
 20 25 30

Asp Leu Thr Met Lys Asp Gly Asn Lys Tyr Asn Ile Asp Glu Ser Thr
 35 40 45

Ser Ser Tyr Arg Glu Val Gly Asp Glu Lys Gly Ser Val Thr Ser Ser
 50 55 60

Ser Leu Val Asp Val Asn Thr Asp Thr Gln Ala Lys Lys Thr Ser Val
 65 70 75 80

His Ser Asp Lys Lys Val Lys Val Asp Lys Pro Lys Ile Ile Pro Pro
 85 90 95

Pro Gly Thr Gly Gln Lys Ile Tyr Glu Ile Asp Pro Leu Leu Gln Ala
 100 105 110

His Arg Gln His Leu Asp Phe Arg Tyr Gly Gln Tyr Lys Arg Ile Arg
 115 120 125

Glu Glu Ile Asp Lys Tyr Glu Gly Gly Leu Asp Ala Phe Ser Arg Gly
 130 135 140

Tyr Glu Lys Phe Gly Phe Thr Arg Ser Ala Thr Gly Ile Thr Tyr Arg
 145 150 155 160

Glu Trp Ala Pro Gly Ala Lys Ser Ala Ala Leu Val Gly Asp Phe Asn
 165 170 175

Asn Trp Asn Pro Asn Ala Asp Val Met Thr Lys Asp Ala Phe Gly Val
 180 185 190

Trp Glu Ile Phe Leu Pro Asn Asn Ala Asp Gly Ser Pro Pro Ile Pro
 195 200 205

His Gly Ser Arg Val Lys Ile His Met Asp Thr Pro Ser Gly Ile Lys
 210 215 220

Asp Ser Ile Pro Ala Trp Ile Lys Phe Ser Val Gln Ala Pro Gly Glu
 225 230 235 240

Ile Pro Tyr Asn Gly Ile Tyr Tyr Asp Pro Pro Glu Glu Glu Lys Tyr
 245 250 255

Val Phe Lys His Pro Gln Pro Lys Arg Pro Gln Ser Ile Arg Ile Tyr
 260 265 270

Glu Ser His Ile Gly Met Ser Ser Pro Glu Pro Lys Ile Asn Thr Tyr
 275 280 285

Ala Asn Phe Arg Asp Asp Val Leu Pro Arg Ile Lys Lys Leu Gly Tyr
 290 295 300

Asn Ala Val Gln Ile Met Ala Ile Gln Glu His Ser Tyr Tyr Ala Ser
 305 310 315 320

Phe Gly Tyr His Val Thr Asn Phe Phe Ala Pro Ser Ser Arg Phe Gly
 325 330 335

Thr Pro Glu Asp Leu Lys Ser Leu Ile Asp Arg Ala His Glu Leu Gly
 340 345 350

Leu Leu Val Leu Met Asp Ile Val His Ser His Ser Ser Asn Asn Thr
 355 360 365

Leu Asp Gly Leu Asn Met Phe Asp Gly Thr Asp Gly His Tyr Phe His
 370 375 380

Pro Gly Ser Arg Gly Tyr His Trp Met Trp Asp Ser Arg Leu Phe Asn
 385 390 395 400

Tyr Gly Ser Trp Glu Val Leu Arg Tyr Leu Leu Ser Asn Ala Arg Trp
 405 410 415

Trp Leu Asp Glu Tyr Lys Phe Asp Gly Phe Arg Phe Asp Gly Val Thr
 420 425 430

Ser Met Met Tyr Thr His His Gly Leu Gln Val Ser Phe Thr Gly Asn
 435 440 445

Tyr Ser Glu Tyr Phe Gly Leu Ala Thr Asp Val Glu Ala Val Val Tyr
 450 455 460

Met Met Leu Val Asn Asp Leu Ile His Gly Leu Phe Pro Glu Ala Val
 465 470 475 480

Ser Ile Gly Glu Asp Val Ser Gly Met Pro Thr Phe Cys Leu Pro Thr
 485 490 495
 Gln Asp Gly Gly Ile Gly Phe Asn Tyr Arg Leu His Met Ala Val Ala
 500 505 510
 Asp Lys Trp Ile Glu Leu Leu Lys Lys Gln Asp Glu Asp Trp Arg Met
 515 520 525
 Gly Asp Ile Val His Thr Leu Thr Asn Arg Arg Trp Leu Glu Lys Cys
 530 535 540
 Val Val Tyr Ala Glu Ser His Asp Gln Ala Leu Val Gly Asp Lys Thr
 545 550 555 560
 Leu Ala Phe Trp Leu Met Asp Lys Asp Met Tyr Asp Phe Met Ala Leu
 565 570 575
 Asp Arg Pro Ser Thr Pro Leu Ile Asp Arg Gly Ile Ala Leu His Lys
 580 585 590
 Met Ile Arg Leu Ile Thr Met Gly Leu Gly Gly Glu Gly Tyr Leu Asn
 595 600 605
 Phe Met Gly Asn Glu Phe Gly His Pro Glu Trp Ile Asp Phe Pro Arg
 610 615 620
 Gly Glu Gln His Leu Pro Asn Gly Lys Ile Val Pro Gly Asn Asn Asn
 625 630 635 640
 Ser Tyr Asp Lys Cys Arg Arg Arg Phe Asp Leu Gly Asp Ala Asp Tyr
 645 650 655
 Leu Arg Tyr His Gly Met Gln Glu Phe Asp Arg Ala Met Gln His Leu
 660 665 670
 Glu Glu Arg Tyr Gly Phe Met Thr Ser Glu His Gln Tyr Ile Ser Arg
 675 680 685
 Lys Asn Glu Gly Asp Arg Val Ile Ile Phe Glu Arg Asp Asn Leu Val
 690 695 700
 Phe Val Phe Asn Phe His Trp Thr Asn Ser Tyr Ser Asp Tyr Lys Val
 705 710 715 720
 Gly Cys Leu Lys Pro Gly Lys Tyr Lys Ile Val Leu Asp Ser Asp Asp
 725 730 735

32

Thr. Leu Phe Gly Gly Phe Asn Arg Leu Asn His Thr Ala Glu Tyr Phe
 740 745 750

Thr Ser Glu Gly Trp Tyr Asp Asp Arg Pro Arg Ser Phe Leu Val Tyr
 755 760 765

Ala Pro Ser Arg Thr Ala Val Val Tyr Ala Leu Ala Asp Gly Val Glu
 770 775 780

Ser Glu Pro Ile Glu Leu Ser Asp Gly Val Glu Ser Glu Pro Ile Glu
 785 790 795 800

Leu Ser Val Gly Val Glu Ser Glu Pro Ile Glu Leu Ser Val Glu Glu
 805 810 815

Ala Glu Ser Glu Pro Ile Glu Arg Ser Val Glu Glu Val Glu Ser Glu
 820 825 830

Thr Thr Gln Gln Ser Val Glu Val Glu Ser Glu Thr Thr Gln Gln Ser
 835 840 845

Val Glu Val Glu Ser Glu Thr Thr Gln
 850 855

<210> 20

<211> 779

<212> PRT

<213> Solanum tuberosum

<400> 20

Thr Met Ala Pro Leu Glu Glu Asp Val Lys Thr Glu Asn Ile Gly Leu
 1 5 10 15

Leu Asn Leu Asp Pro Thr Leu Glu Pro Tyr Leu Asp His Phe Arg His
 20 25 30

Arg Met Lys Arg Tyr Val Asp Gln Lys Met Leu Ile Glu Lys Tyr Glu
 35 40 45

Gly Pro Leu Glu Glu Phe Ala Gln Gly Tyr Leu Lys Phe Gly Phe Asn
 50 55 60

Arg Glu Asp Gly Cys Ile Val Tyr Arg Glu Trp Ala Pro Ala Ala Gln
 65 70 75 80

Glu Asp Glu Val Ile Gly Asp Phe Asn Gly Trp Asn Gly Ser Asn His
 85 90 95

Met Met Glu Lys Asp Gln Phe Gly Val Trp Ser Ile Arg Ile Pro Asp
 100 105 110

Val Asp Ser Lys Pro Val Ile Pro His Asn Ser Arg Val Lys Phe Arg
 115 120 125

Phe Lys His Gly Asn Gly Val Trp Val Asp Arg Ile Pro Ala Trp Ile
 130 135 140

Lys Tyr Ala Thr Ala Asp Ala Thr Lys Phe Ala Ala Pro Tyr Asp Gly
 145 150 155 160

Val Tyr Trp Asp Pro Pro Pro Ser Glu Arg Tyr His Phe Lys Tyr Pro
 165 170 175

Arg Pro Pro Lys Pro Arg Ala Pro Arg Ile Tyr Glu Ala His Val Gly
 180 185 190

Met Ser Ser Ser Glu Pro Arg Val Asn Ser Tyr Arg Glu Phe Ala Asp
 195 200 205

Asp Val Leu Pro Arg Ile Lys Ala Asn Asn Tyr Asn Thr Val Gln Leu
 210 215 220

Met Ala Ile Met Glu His Ser Tyr Tyr Gly Ser Phe Gly Tyr His Val
 225 230 235 240

Thr Asn Phe Phe Ala Val Ser Ser Arg Tyr Gly Asn Pro Glu Asp Leu
 245 250 255

Lys Tyr Leu Ile Asp Lys Ala His Ser Leu Gly Leu Gln Val Leu Val
 260 265 270

Asp Val Val His Ser His Ala Ser Asn Asn Val Thr Asp Gly Leu Asn
 275 280 285

Gly Phe Asp Ile Gly Gln Gly Ser Gln Glu Ser Tyr Phe His Ala Gly
 290 295 300

Glu Arg Gly Tyr His Lys Leu Trp Asp Ser Arg Leu Phe Asn Tyr Ala
 305 310 315 320

Asn Trp Glu Val Leu Arg Phe Leu Leu Ser Asn Leu Arg Trp Trp Leu
 325 330 335

Glu Glu Tyr Asn Phe Asp Gly Phe Arg Phe Asp Gly Ile Thr Ser Met
 340 345 350

Leu Tyr Val His His Gly Ile Asn Met Gly Phe Thr Gly Asn Tyr Asn
 355 360 365
 Glu Tyr Phe Ser Glu Ala Thr Asp Val Asp Ala Val Val Tyr Leu Met
 370 375 380
 Leu Ala Asn Asn Leu Ile His Lys Ile Phe Pro Asp Ala Thr Val Ile
 385 390 395 400
 Ala Glu Asp Val Ser Gly Met Pro Gly Leu Gly Arg Pro Val Ser Glu
 405 410 415
 Gly Gly Ile Gly Phe Asp Tyr Arg Leu Ala Met Ala Ile Pro Asp Lys
 420 425 430
 Trp Ile Asp Tyr Leu Lys Asn Lys Asn Asp Glu Asp Trp Ser Met Lys
 435 440 445
 Glu Val Thr Ser Ser Leu Thr Asn Arg Arg Tyr Thr Glu Lys Cys Ile
 450 455 460
 Ala Tyr Ala Glu Ser His Asp Gln Ser Ile Val Gly Asp Lys Thr Ile
 465 470 475 480
 Ala Phe Leu Leu Met Asp Lys Glu Met Tyr Ser Gly Met Ser Cys Leu
 485 490 495
 Thr Asp Ala Ser Pro Val Val Asp Arg Gly Ile Ala Leu His Lys Met
 500 505 510
 Ile His Phe Phe Thr Met Ala Leu Gly Gly Glu Gly Tyr Leu Asn Phe
 515 520 525
 Met Gly Asn Glu Phe Gly His Pro Glu Trp Ile Asp Phe Pro Arg Glu
 530 535 540
 Gly Asn Asn Trp Ser Tyr Asp Lys Cys Arg Arg Gln Trp Asn Leu Ala
 545 550 555 560
 Asp Ser Glu His Leu Arg Tyr Lys Phe Met Asn Ala Phe Asp Arg Ala
 565 570 575
 Met Asn Ser Leu Asp Glu Lys Phe Ser Phe Leu Ala Ser Gly Lys Gln
 580 585 590
 Ile Val Ser Ser Met Asp Asp Asp Asn Lys Val Val Val Phe Glu Arg
 595 600 605

Gly Asp Leu Val Phe Val Phe Asn Phe His Pro Lys Asn Thr Tyr Glu
 610 615 620

Gly Tyr Lys Val Gly Cys Asp Leu Pro Gly Lys Tyr Arg Val Ala Leu
 625 630 635 640

Asp Ser Asp Ala Trp Glu Phe Gly Gly His Gly Arg Thr Gly His Asp
 645 650 655

Val Asp His Phe Thr Ser Pro Glu Gly Ile Pro Gly Val Pro Glu Thr
 660 665 670

Asn Phe Asn Gly Arg Gln Ile Pro Ser Lys Cys Cys Leu Leu Arg Glu
 675 680 685

His Val Trp Leu Ile Thr Glu Leu Met Asn Ala Cys Gln Lys Leu Lys
 690 695 700

Ile Thr Arg Gln Thr Phe Val Val Ser Tyr Tyr Gln Gln Pro Ile Ser
 705 710 715 720

Arg Arg Val Thr Arg Asn Leu Lys Ile Arg Tyr Leu Gln Ile Ser Val
 725 730 735

Thr Leu Thr Asn Ala Cys Gln Lys Leu Lys Phe Thr Arg Gln Thr Phe
 740 745 750

Leu Val Ser Tyr Tyr Gln Gln Pro Ile Leu Arg Arg Val Thr Arg Lys
 755 760 765

Leu Lys Asp Ser Leu Ser Thr Asn Ile Ser Thr
 770 775

<210> 21

<211> 762

<212> PRT

<213> Triticum aestivum

<400> 21

Thr Met Ala Thr Ala Glu Asp Gly Val Gly Asp Leu Pro Ile Tyr Asp
 1 5 10 15

Leu Asp Pro Lys Phe Ala Gly Phe Lys Glu His Phe Ser Tyr Arg Met
 20 25 30

36

Lys Lys Tyr Leu Asp Gln Lys His Ser Ile Glu Lys His Glu Gly Gly
 35 40 45

Leu Glu Glu Phe Ser Lys Gly Tyr Leu Lys Phe Gly Ile Asn Thr Glu
 50 55 60

Asn Asp Ala Thr Val Tyr Arg Glu Trp Ala Pro Ala Ala Met Asp Ala
 65 70 75 80

Gln Leu Ile Gly Asp Phe Asn Asn Trp Asn Gly Ser Gly His Arg Met
 85 90 95

Thr Lys Asp Asn Tyr Gly Val Trp Ser Ile Arg Ile Ser His Val Asn
 100 105 110

Gly Lys Pro Ala Ile Pro His Asn Ser Lys Val Lys Phe Arg Phe His
 115 120 125

Arg Gly Asp Gly Leu Trp Val Asp Arg Val Pro Ala Trp Ile Arg Tyr
 130 135 140

Ala Thr Phe Asp Ala Ser Lys Phe Gly Ala Pro Tyr Asp Gly Val His
 145 150 155 160

Trp Asp Pro Pro Ser Gly Glu Arg Tyr Val Phe Lys His Pro Arg Pro
 165 170 175

Arg Lys Pro Asp Ala Pro Arg Ile Tyr Glu Ala His Val Gly Met Ser
 180 185 190

Gly Glu Lys Pro Glu Val Ser Thr Tyr Arg Glu Phe Ala Asp Asn Val
 195 200 205

Leu Pro Arg Ile Lys Ala Asn Asn Tyr Asn Thr Val Gln Leu Met Ala
 210 215 220

Ile Met Glu His Ser Tyr Tyr Ala Ser Phe Gly Tyr His Val Thr Asn
 225 230 235 240

Phe Phe Ala Val Ser Ser Arg Ser Gly Thr Pro Glu Asp Leu Lys Tyr
 245 250 255

Leu Val Asp Lys Ala His Ser Leu Gly Leu Arg Val Leu Met Asp Val
 260 265 270

Val His Ser His Ala Ser Ser Asn Lys Thr Asp Gly Leu Asn Gly Tyr
 275 280 285

Asp Val Gly Gln Asn Thr Gln Glu Ser Tyr Phe His Thr Gly Glu Arg
 290 295 300

Gly Tyr His Lys Leu Trp Asp Ser Arg Leu Phe Asn Tyr Ala Asn Trp
 305 310 315 320

Glu Val Leu Arg Phe Leu Leu Ser Asn Leu Arg Tyr Trp Met Asp Glu
 325 330 335

Phe Met Phe Asp Gly Phe Arg Phe Asp Gly Val Thr Ser Met Leu Tyr
 340 345 350

Asn His His Gly Ile Asn Met Ser Phe Ala Gly Ser Tyr Lys Glu Tyr
 355 360 365

Phe Gly Leu Asp Thr Asp Val Asp Ala Val Val Tyr Leu Met Leu Ala
 370 375 380

Asn His Leu Met His Lys Leu Leu Pro Glu Ala Thr Val Val Ala Glu
 385 390 395 400

Asp Val Ser Gly Met Pro Val Leu Cys Arg Ser Val Asp Glu Gly Gly
 405 410 415

Val Gly Phe Asp Tyr Arg Leu Ala Met Ala Ile Pro Asp Arg Trp Ile
 420 425 430

Asp Tyr Leu Lys Asn Lys Asp Asp Leu Glu Trp Ser Met Ser Gly Ile
 435 440 445

Ala His Thr Leu Thr Asn Arg Arg Tyr Thr Glu Lys Cys Ile Ala Tyr
 450 455 460

Ala Glu Ser His Asp Gln Ser Ile Val Gly Asp Lys Thr Met Ala Phe
 465 470 475 480

Leu Leu Met Asp Lys Glu Met Tyr Thr Gly Met Ser Asp Leu Gln Pro
 485 490 495

Ala Ser Pro Thr Ile Asp Arg Gly Ile Ala Leu Gln Lys Met Ile His
 500 505 510

Phe Ile Thr Met Ala Leu Gly Gly Asp Gly Tyr Leu Asn Phe Met Gly
 515 520 525

Asn Glu Phe Gly His Pro Glu Trp Ile Asp Phe Pro Arg Glu Gly Asn
 530 535 540

Asn Trp Ser Tyr Asp Lys Cys Arg Arg Gln Trp Ser Leu Ala Asp Ile
 545 550 555 560
 Asp His Leu Arg Tyr Lys Tyr Met Asn Ala Phe Asp Gln Ala Met Asn
 565 570 575
 Ala Leu Asp Asp Lys Phe Ser Phe Leu Ser Ser Ser Lys Gln Ile Val
 580 585 590
 Ser Asp Met Asn Glu Glu Lys Lys Ile Ile Val Phe Glu Arg Gly Asp
 595 600 605
 Leu Val Phe Val Phe Asn Phe His Pro Ser Lys Thr Tyr Asp Gly Tyr
 610 615 620
 Lys Val Gly Cys Asp Leu Pro Gly Lys Tyr Lys Val Ala Leu Asp Ser
 625 630 635 640
 Asp Ala Leu Met Phe Gly Gly His Gly Arg Val Ala His Asp Asn Asp
 645 650 655
 His Phe Thr Ser Pro Glu Gly Val Pro Gly Val Pro Glu Thr Asn Phe
 660 665 670
 Asn Asn Arg Pro Asn Ser Phe Lys Ile Leu Ser Pro Ser Arg Thr Cys
 675 680 685
 Val Ala Tyr Tyr Arg Val Glu Glu Lys Ala Glu Lys Pro Lys Asp Glu
 690 695 700
 Gly Ala Ala Ser Trp Gly Lys Thr Ala Leu Gly Tyr Ile Asp Val Glu
 705 710 715 720
 Ala Thr Gly Val Lys Asp Ala Ala Asp Gly Glu Ala Thr Ser Gly Ser
 725 730 735
 Glu Lys Ala Ser Thr Gly Gly Asp Ser Ser Lys Lys Gly Ile Asn Phe
 740 745 750
 Val Phe Leu Ser Pro Asp Lys Asp Asn Lys
 755 760

<210> 22

<211> 703

<212> PRT

<213> Triticum aestivum

<400> 22

Ser Pro Pro Thr Leu Thr Ser Pro Pro Pro Ser Ala Val Pro Ser Thr
 1 5 10 15

Thr Met Leu Cys Leu Ser Ser Ser Leu Leu Pro Arg Pro Ser Ala Ala
 20 25 30

Ala Asp Arg Pro Leu Pro Gly Ile Ile Ala Gly Gly Gly Gly Gly Lys
 35 40 45

Arg Leu Ser Val Val Pro Ser Val Pro Phe Leu Leu Arg Trp Leu Trp
 50 55 60

Pro Arg Lys Ala Lys Ser Lys Ser Phe Val Ser Val Thr Ala Arg Gly
 65 70 75 80

Asn Lys Ile Ala Ala Thr Thr Gly Tyr Gly Ser Asp His Leu Pro Ile
 85 90 95

Tyr Asp Leu Asp Leu Lys Leu Ala Glu Phe Lys Asp His Phe Asp Tyr
 100 105 110

Thr Arg Asn Arg Tyr Ile Glu Gln Lys His Leu Ile Glu Lys His Glu
 115 120 125

Gly Ser Leu Glu Glu Phe Ser Lys Gly Tyr Leu Lys Phe Gly Ile Asn
 130 135 140

Thr Glu His Gly Ala Ser Val Tyr Arg Glu Trp Ala Pro Ala Ala Glu
 145 150 155 160

Glu Ala Gln Leu Val Gly Asp Phe Asn Asn Trp Asn Gly Ser Gly His
 165 170 175

Lys Met Ala Lys Asp Asn Phe Gly Val Trp Ser Ile Arg Ile Ser His
 180 185 190

Val Asn Gly Lys Pro Ala Ile Pro His Asn Ser Lys Val Lys Phe Arg
 195 200 205

Phe Arg His His Gly Val Trp Val Glu Gln Ile Pro Ala Trp Ile Arg
 210 215 220

Tyr Ala Thr Val Thr Ala Ser Glu Ser Gly Ala Pro Tyr Asp Gly Leu
 225 230 235 240

His Trp Asp Pro Pro Ser Ser Glu Arg Tyr Val Phe Asn His Pro Arg
 245 250 255

40

Pro Pro Lys Pro Asp Val Pro Arg Ile Tyr Glu Ala His Val Gly Val
 260 265 270

Ser Gly Gly Lys Leu Glu Ala Gly Thr Tyr Arg Glu Phe Pro Asp Asn
 275 280 285

Val Leu Pro Cys Leu Arg Ala Thr Asn Tyr Asn Thr Val Gln Leu Met
 290 295 300

Gly Ile Met Glu His Ser Asp Ser Ala Ser Phe Gly Tyr His Val Thr
 305 310 315 320

Asn Phe Phe Ala Val Ser Ser Arg Ser Gly Thr Pro Glu Asp Leu Lys
 325 330 335

Tyr Leu Ile Asp Lys Ala His Ser Leu Gly Leu Arg Val Leu Met Asp
 340 345 350

Val Val His Ser His Ala Ser Asn Asn Val Ile Asp Gly Leu Asn Gly
 355 360 365

Tyr Asp Val Gly Gln Ser Ala His Glu Ser Tyr Phe Tyr Thr Gly Asp
 370 375 380

Lys Gly Tyr Asn Lys Met Trp Asn Gly Arg Met Phe Asn Tyr Ala Asn
 385 390 395 400

Trp Glu Val Leu Arg Phe Leu Leu Ser Asn Leu Arg Tyr Trp Met Asp
 405 410 415

Glu Phe Met Phe Asp Gly Phe Arg Phe Val Gly Val Thr Ser Met Leu
 420 425 430

Tyr Asn His Asn Gly Ile Asn Met Ser Phe Asn Gly Asn Tyr Lys Asp
 435 440 445

Tyr Ile Gly Leu Asp Thr Asn Val Asp Ala Phe Val Tyr Met Met Leu
 450 455 460

Ala Asn His Leu Met His Lys Leu Phe Pro Glu Ala Ile Val Val Ala
 465 470 475 480

Val Asp Val Ser Gly Met Pro Val Leu Cys Trp Pro Val Asp Glu Gly
 485 490 495

Gly Leu Gly Phe Asp Tyr Arg Gln Ala Met Thr Ile Pro Asp Arg Trp
 500 505 510

Ile Asp Tyr Leu Glu Asn Lys Gly Asp Gln Gln Trp Ser Met Ser Ser
 515 520 525

Val Ile Ser Gln Thr Leu Thr Asn Arg Arg Tyr Pro Glu Lys Phe Ile
 530 535 540

Ala Tyr Ala Glu Arg Gln Asn His Ser Ile Ile Gly Ser Lys Thr Met
 545 550 555 560

Ala Phe Leu Leu Met Glu Trp Glu Thr Tyr Ser Gly Met Ser Ala Met
 565 570 575

Asp Pro Asp Ser Pro Thr Ile Asp Arg Ala Ile Ala Leu Gln Lys Met
 580 585 590

Ile His Phe Ile Thr Met Ala Phe Gly Gly Asp Ser Tyr Leu Lys Phe
 595 600 605

Met Gly Asn Glu Tyr Met Asn Ala Phe Val Gln Ala Val Asp Thr Pro
 610 615 620

Ser Asp Lys Cys Ser Phe Leu Ser Ser Ser Asn Gln Thr Ala Ser His
 625 630 635 640

Met Asn Glu Glu Glu Lys Gly Ser Ala Leu Thr Lys Gly Tyr Thr His
 645 650 655

Leu Arg Ser Gly Cys Phe Asp Pro Ser Leu Pro Ser Thr Ser Ser Cys
 660 665 670

Ala Phe Leu Gly Pro Ser Asn Gln Ser Pro Phe Ser Lys Pro Phe Ile
 675 680 685

Gly Phe Pro Gly Cys Ile Phe Cys Cys Gly Leu Phe Lys Gly Glu
 690 695 700

<210> 23

<211> 752

<212> PRT

<213> Zea mays

<400> 23

Thr Met Ala Thr Ala Lys Gly Asp Val Asp His Leu Pro Ile Tyr Asp
 1 5 10 15

Leu Asp Pro Lys Leu Glu Ile Phe Lys Asp His Phe Arg Tyr Arg Met

	20	42	25	30
Lys Arg Phe Leu Glu Gln Lys Gly Ser Ile Glu Glu Asn Glu Gly Ser	35	40	45	
Leu Glu Ser Phe Ser Lys Gly Tyr Leu Lys Phe Gly Ile Asn Thr Asn	50	55	60	
Glu Asp Gly Thr Val Tyr Arg Glu Trp Ala Pro Ala Ala Gln Glu Ala	65	70	75	80
Glu Leu Ile Gly Asp Phe Asn Asp Trp Asn Gly Ala Asn His Lys Met	85	90	95	
Glu Lys Asp Lys Phe Gly Val Trp Ser Ile Lys Ile Asp His Val Lys	100	105	110	
Gly Lys Pro Ala Ile Pro His Asn Ser Lys Val Lys Phe Arg Phe Leu	115	120	125	
His Gly Gly Val Trp Val Asp Arg Ile Pro Ala Leu Ile Arg Tyr Ala	130	135	140	
Thr Val Asp Ala Ser Lys Phe Gly Ala Pro Tyr Asp Gly Val His Trp	145	150	155	160
Asp Pro Pro Ala Ser Glu Arg Tyr Thr Phe Lys His Pro Arg Pro Ser	165	170	175	
Lys Pro Ala Ala Pro Arg Ile Tyr Glu Ala His Val Gly Met Ser Gly	180	185	190	
Glu Lys Pro Ala Val Ser Thr Tyr Arg Glu Phe Ala Asp Asn Val Leu	195	200	205	
Pro Arg Ile Arg Ala Asn Asn Tyr Asn Thr Val Gln Leu Met Ala Val	210	215	220	
Met Glu His Ser Tyr Tyr Ala Ser Phe Gly Tyr His Val Thr Asn Phe	225	230	235	240
Phe Ala Val Ser Ser Arg Ser Gly Thr Pro Glu Asp Leu Lys Tyr Leu	245	250	255	
Val Asp Lys Ala His Ser Leu Gly Leu Arg Val Leu Met Asp Val Val	260	265	270	
His Ser His Ala Ser Asn Asn Val Thr Asp Gly Leu Asn Gly Tyr Asp				

275	280	43	285
Val Gly Gln Ser Thr Gln Glu Ser Tyr Phe His Ala Gly Asp Arg Gly			
290	295		300
Tyr His Lys Leu Trp Asp Ser Arg Leu Phe Asn Tyr Ala Asn Trp Glu			
305	310	315	320
Val Leu Arg Phe Leu Leu Ser Asn Leu Arg Tyr Trp Leu Asp Glu Phe			
	325	330	335
Met Phe Asp Gly Phe Arg Phe Asp Gly Val Thr Ser Met Leu Tyr His			
	340	345	350
His His Gly Ile Asn Val Gly Phe Thr Gly Asn Tyr Gln Glu Tyr Phe			
	355	360	365
Ser Leu Asp Thr Ala Val Asp Ala Val Val Tyr Met Met Leu Ala Asn			
370	375	380	
His Leu Met His Lys Leu Leu Pro Glu Ala Thr Val Val Ala Glu Asp			
385	390	395	400
Val Ser Gly Met Pro Val Leu Cys Arg Pro Val Asp Glu Gly Gly Val			
	405	410	415
Gly Phe Asp Tyr Arg Leu Ala Met Ala Ile Pro Asp Arg Trp Ile Asp			
	420	425	430
Tyr Leu Lys Asn Lys Asp Asp Ser Glu Trp Ser Met Gly Glu Ile Ala			
	435	440	445
His Thr Leu Thr Asn Arg Arg Tyr Thr Glu Lys Cys Ile Ala Tyr Ala			
450	455	460	
Glu Ser His Asp Gln Ser Ile Val Gly Asp Lys Thr Ile Ala Phe Leu			
465	470	475	480
Leu Met Asp Lys Glu Met Tyr Thr Gly Met Ser Asp Leu Gln Pro Ala			
	485	490	495
Ser Pro Thr Ile Asp Arg Gly Ile Ala Leu Gln Lys Met Ile His Phe			
	500	505	510
Ile Thr Met Ala Leu Gly Gly Asp Gly Tyr Leu Asn Phe Met Gly Asn			
	515	520	525
Glu Phe Gly His Pro Glu Trp Ile Asp Phe Pro Arg Glu Gly Asn Asn			

530 535 540
 Trp Ser Tyr Asp Lys Cys Arg Arg Gln Trp Ser Leu Val Asp Thr Asp
 545 550 555 560
 His Leu Arg Tyr Lys Tyr Met Asn Ala Phe Asp Gln Ala Met Asn Ala
 565 570 575
 Leu Asp Glu Arg Phe Ser Phe Leu Ser Ser Ser Lys Gln Ile Val Ser
 580 585 590
 Asp Met Asn Asp Glu Glu Lys Val Ile Val Phe Glu Arg Gly Asp Leu
 595 600 605
 Val Phe Val Phe Asn Phe His Pro Lys Lys Thr Tyr Glu Gly Tyr Lys
 610 615 620
 Val Gly Cys Asp Leu Pro Gly Lys Tyr Arg Val Ala Leu Asp Ser Asp
 625 630 635 640
 Ala Leu Val Phe Gly Gly His Gly Arg Val Gly His Asp Val Asp His
 645 650 655
 Phe Thr Ser Pro Glu Gly Val Pro Gly Val Pro Glu Thr Asn Phe Asn
 660 665 670
 Asn Arg Pro Asn Ser Phe Lys Val Leu Ser Pro Pro Arg Thr Cys Val
 675 680 685
 Ala Tyr Tyr Arg Val Asp Glu Ala Gly Ala Gly Arg Arg Leu His Ala
 690 695 700
 Lys Ala Glu Thr Gly Lys Thr Ser Pro Ala Glu Ser Ile Asp Val Lys
 705 710 715 720
 Ala Ser Arg Ala Ser Ser Lys Glu Asp Lys Glu Ala Thr Ala Gly Gly
 725 730 735
 Lys Lys Gly Trp Lys Phe Ala Arg Gln Pro Ser Asp Gln Asp Thr Lys
 740 745 750

<210> 24

<211> 756

<212> PRT

<213> Oryza sativa

45

<400> 24

Thr Met Val Thr Val Val Glu Glu Val Asp His Leu Pro Ile Tyr Asp
 1 5 10 15
 Leu Asp Pro Lys Leu Glu Glu Phe Lys Asp His Phe Asn Tyr Arg Ile
 20 25 30
 Lys Arg Tyr Leu Asp Gln Lys Cys Leu Ile Glu Lys His Glu Gly Gly
 35 40 45
 Leu Glu Glu Phe Ser Lys Gly Tyr Leu Lys Phe Gly Ile Asn Thr Val
 50 55 60
 Asp Gly Ala Thr Ile Tyr Arg Glu Trp Ala Pro Ala Ala Gln Glu Ala
 65 70 75 80
 Gln Leu Ile Gly Glu Phe Asn Asn Trp Asn Gly Ala Lys His Lys Met
 85 90 95
 Glu Lys Asp Lys Phe Gly Ile Trp Ser Ile Lys Ile Ser His Val Asn
 100 105 110
 Gly Lys Pro Ala Ile Pro His Asn Ser Lys Val Lys Phe Arg Phe Arg
 115 120 125
 His Gly Gly Gly Ala Trp Val Asp Arg Ile Pro Ala Trp Ile Arg Tyr
 130 135 140
 Ala Thr Phe Asp Ala Ser Lys Phe Gly Ala Pro Tyr Asp Gly Val His
 145 150 155 160
 Trp Asp Pro Pro Ala Cys Glu Arg Tyr Val Phe Lys His Pro Arg Pro
 165 170 175
 Pro Lys Pro Asp Ala Pro Arg Ile Tyr Glu Ala His Val Gly Met Ser
 180 185 190
 Gly Glu Glu Pro Glu Val Ser Thr Tyr Arg Glu Phe Ala Asp Asn Val
 195 200 205
 Leu Pro Arg Ile Arg Ala Asn Asn Tyr Asn Thr Val Gln Leu Met Ala
 210 215 220
 Ile Met Glu His Ser Tyr Tyr Ala Ser Phe Gly Tyr His Val Thr Asn
 225 230 235 240

46

Phe Phe Ala Val Ser Ser Arg Ser Gly Thr Pro Glu Asp Leu Lys Tyr
 245 250 255

Leu Val Asp Lys Ala His Ser Leu Gly Leu Arg Val Leu Met Asp Val
 260 265 270

Val His Ser His Ala Ser Asn Asn Val Thr Asp Gly Leu Asn Gly Tyr
 275 280 285

Asp Val Gly Gln Asn Thr His Glu Ser Tyr Phe His Thr Gly Asp Arg
 290 295 300

Gly Tyr His Lys Leu Trp Asp Ser Arg Leu Phe Asn Tyr Ala Asn Trp
 305 310 315 320

Glu Val Leu Arg Phe Leu Leu Ser Asn Leu Arg Tyr Trp Met Asp Glu
 325 330 335

Phe Met Phe Asp Gly Phe Arg Phe Asp Gly Val Thr Ser Met Leu Tyr
 340 345 350

His His His Gly Ile Asn Lys Gly Phe Thr Gly Asn Tyr Lys Glu Tyr
 355 360 365

Phe Ser Leu Asp Thr Asp Val Asp Ala Ile Val Tyr Met Met Leu Ala
 370 375 380

Asn His Leu Met His Lys Leu Leu Pro Glu Ala Thr Ile Val Ala Glu
 385 390 395 400

Asp Val Ser Gly Met Pro Val Leu Cys Arg Pro Val Asp Glu Gly Gly
 405 410 415

Val Gly Phe Asp Phe Arg Leu Ala Met Ala Ile Pro Asp Arg Trp Ile
 420 425 430

Asp Tyr Leu Lys Asn Lys Glu Asp Arg Lys Trp Ser Met Ser Glu Ile
 435 440 445

Val Gln Thr Leu Thr Asn Arg Arg Tyr Thr Glu Lys Cys Ile Ala Tyr
 450 455 460

Ala Glu Ser His Asp Gln Ser Ile Val Gly Asp Lys Thr Ile Ala Phe
 465 470 475 480

Leu Leu Met Asp Lys Glu Met Tyr Thr Gly Met Ser Asp Leu Gln Pro
 485 490 495

Ala Ser Pro Thr Ile Asn Arg Gly Ile Ala Leu Gln Lys Met Ile His
 500 505 510

Phe Ile Thr Met Ala Leu Gly Gly Asp Gly Tyr Leu Asn Phe Met Gly
 515 520 525

Asn Glu Phe Gly His Pro Glu Trp Ile Asp Phe Pro Arg Glu Gly Asn
 530 535 540

Asn Trp Ser Tyr Asp Lys Cys Arg Arg Gln Trp Ser Leu Val Asp Thr
 545 550 555 560

Asp His Leu Arg Tyr Lys Tyr Met Asn Ala Phe Asp Gln Ala Met Asn
 565 570 575

Ala Leu Glu Glu Glu Phe Ser Phe Leu Ser Ser Ser Lys Gln Ile Val
 580 585 590

Ser Asp Met Asn Glu Lys Asp Lys Val Ile Val Phe Glu Arg Gly Asp
 595 600 605

Leu Val Phe Val Phe Asn Phe His Pro Asn Lys Thr Tyr Lys Gly Tyr
 610 615 620

Lys Val Gly Cys Asp Leu Pro Gly Lys Tyr Arg Val Ala Leu Asp Ser
 625 630 635 640

Asp Ala Leu Val Phe Gly Gly His Gly Arg Val Gly His Asp Val Asp
 645 650 655

His Phe Thr Ser Pro Glu Gly Met Pro Gly Val Pro Glu Thr Asn Phe
 660 665 670

Asn Asn Arg Pro Asn Ser Phe Lys Val Leu Ser Pro Pro Arg Thr Cys
 675 680 685

Val Ala Tyr Tyr Arg Val Asp Glu Asp Arg Glu Glu Leu Arg Arg Gly
 690 695 700

Gly Ala Val Ala Ser Gly Lys Ile Val Thr Glu Tyr Ile Asp Val Glu
 705 710 715 720

Ala Thr Ser Gly Glu Thr Ile Ser Gly Gly Trp Lys Gly Ser Glu Lys
 725 730 735

Asp Asp Cys Gly Lys Lys Gly Met Lys Phe Val Phe Arg Ser Ser Asp
 740 745 750

Glu Asp Cys Lys
755

48

<210> 25
<211> 762
<212> PRT
<213> Pisum sativum

<400> 25

Thr Met Pro Ser Val Glu Glu Asp Phe Glu Asn Ile Gly Ile Leu Asn
1 5 10 15

Val Asp Ser Ser Leu Glu Pro Phe Lys Asp His Phe Lys Tyr Arg Leu
20 25 30

Lys Arg Tyr Leu His Gln Lys Lys Leu Ile Glu Glu Tyr Glu Gly Gly
35 40 45

Leu Gln Glu Phe Ala Lys Gly Tyr Leu Lys Phe Gly Phe Asn Arg Glu
50 55 60

Glu Asp Gly Ile Ser Tyr Arg Glu Trp Ala Pro Ala Ala Gln Glu Ala
65 70 75 80

Gln Ile Ile Gly Asp Phe Asn Gly Trp Asn Gly Ser Asn Leu His Met
85 90 95

Glu Lys Asp Gln Phe Gly Val Trp Ser Ile Gln Ile Pro Asp Ala Asp
100 105 110

Gly Asn Pro Ala Ile Pro His Asn Ser Arg Val Lys Phe Arg Phe Lys
115 120 125

His Ser Asp Gly Val Trp Val Asp Arg Ile Pro Ala Trp Ile Lys Tyr
130 135 140

Ala Thr Val Asp Pro Thr Arg Phe Ala Ala Pro Tyr Asp Gly Val Tyr
145 150 155 160

Trp Asp Pro Pro Leu Ser Glu Arg Tyr Gln Phe Lys His Pro Arg Pro
165 170 175

Pro Lys Pro Lys Ala Pro Arg Ile Tyr Glu Ala His Val Gly Met Ser
180 185 190

Ser Ser Glu Pro Arg Ile Asn Ser Tyr Arg Glu Phe Ala Asp Asp Val
195 200 205

Leu Pro Arg Ile Arg Glu Asn Asn Tyr Asn Thr Val Gln Leu Met Ala
 210 215 220
 Val Met Glu His Ser Tyr Tyr Ala Ser Phe Trp Tyr His Val Thr Lys
 225 230 235 240
 Pro Phe Phe Ala Val Ser Ser Arg Ser Gly Ser Pro Glu Asp Leu Lys
 245 250 255
 Tyr Leu Ile Asp Lys Ala His Ser Leu Gly Leu Asn Val Leu Met Asp
 260 265 270
 Val Ile His Ser His Ala Ser Asn Asn Val Thr Asp Gly Leu Asn Gly
 275 280 285
 Phe Asp Val Gly Gln Ser Ser Gln Gln Ser Tyr Phe His Ala Gly Asp
 290 295 300
 Arg Gly Tyr His Lys Leu Trp Asp Ser Arg Leu Phe Asn Tyr Ala Asn
 305 310 315 320
 Trp Lys Ser Ser Phe Leu Leu Ser Asn Leu Arg Trp Trp Leu Glu Glu
 325 330 335
 Tyr Lys Phe Asp Gly Phe Arg Phe Asp Gly Val Thr Ser Met Leu Tyr
 340 345 350
 His His His Gly Ile Asn Met Ala Phe Thr Gly Asp Tyr Asn Glu Tyr
 355 360 365
 Phe Ser Glu Glu Thr Asp Val Asp Ala Val Val Tyr Leu Met Leu Ala
 370 375 380
 Asn Ser Leu Val His Asp Ile Leu Pro Asp Ala Thr Asp Ile Ala Glu
 385 390 395 400
 Asp Val Ser Gly Met Pro Gly Leu Gly Arg Pro Val Ser Glu Val Gly
 405 410 415
 Ile Gly Phe Asp Tyr Arg Leu Ala Met Ala Ile Pro Asp Lys Trp Ile
 420 425 430
 Asp Tyr Leu Lys Asn Lys Lys Asp Ser Glu Trp Ser Met Lys Glu Ile
 435 440 445
 Ser Leu Asn Leu Thr Asn Arg Arg Tyr Thr Glu Lys Cys Val Ser Tyr
 450 455 460

Ala Glu Ser His Asp Gln Ser Ile Val Gly Asp Lys Thr Ile Ala Phe
 465 470 475 480

Leu Leu Met Asp Glu Glu Met Tyr Ser Ser Met Ser Cys Leu Thr Met
 485 490 495

Leu Ser Pro Thr Ile Glu Arg Gly Ile Ser Leu His Lys Met Ile His
 500 505 510

Phe Ile Thr Leu Ala Leu Gly Gly Glu Gly Tyr Leu Asn Phe Met Gly
 515 520 525

Asn Glu Phe Gly His Pro Glu Trp Ile Asp Phe Pro Arg Glu Gly Asn
 530 535 540

Gly Trp Ser Tyr Glu Lys Cys Arg Leu Thr Gln Trp Asn Leu Val Asp
 545 550 555 560

Thr Asn His Leu Arg Tyr Lys Phe Met Asn Ala Phe Asp Arg Ala Met
 565 570 575

Asn Leu Leu Asp Asp Lys Phe Ser Ile Leu Ala Ser Thr Lys Gln Ile
 580 585 590

Val Ser Ser Thr Asn Asn Glu Asp Lys Val Ile Val Phe Glu Arg Gly
 595 600 605

Asp Leu Val Phe Val Phe Asn Phe His Pro Glu Asn Thr Tyr Glu Gly
 610 615 620

Tyr Lys Val Gly Cys Asp Leu Pro Gly Lys Tyr Arg Val Ala Leu Asp
 625 630 635 640

Ser Asp Ala Thr Glu Phe Gly Gly His Gly Arg Val Gly His Asp Ala
 645 650 655

Asp Gln Phe Thr Ser Pro Glu Gly Ile Pro Gly Ile Pro Glu Thr Asn
 660 665 670

Phe Asn Asn Arg Pro Asn Ser Phe Lys Val Leu Ser Pro Pro His Thr
 675 680 685

Cys Val Val Tyr Tyr Arg Val Asp Glu Arg Gln Glu Glu Ser Asn Asn
 690 695 700

Pro Asn Leu Gly Ser Val Glu Glu Thr Phe Ala Ala Ala Asp Thr Asp
 705 710 715 720

tccactggag caatagcttt ttgactacc gtgttgggtg ttccaagcct gggaagtaca 480
 aggtggcctt agactccgac gatgcactct ttggtggatt gagcaggctt gatcatgatg 540
 tcgactactt cacaaccgaa catccgcatg acaataggcc gcgctctttc ttggtgtaca 600
 ctctagcag aactgcggtc gtgtatgccc ttacagagta agaaccagca gcggcttgtt 660
 acaaggcaaa gagagaactc caggagctc gtggattgtg agcgaagcga cgggcaactg 720
 cgtgaggctg ctctaagcgc catgactggg aggggatcgt gcctcttccc ctgatgccag 780
 gaggatcaga tggataggta gcttgttggt gagcgctcga aagaaaatgg acgggcctgg 840
 gtgtttgtcg tgctgcactt aaccctcctc ctatgttgca cattccccggg tgtttttgta 900
 catataacta ataattgccc gtgcgcttca acatgaacat ataaatattc tatataaaaa 960
 aaaaaaaaaa aaaaaaa 977

<210> 28

<211> 212

<212> PRT

<213> Triticum aestivum

<400> 28

Met Tyr Asp Phe Met Ala Leu Asp Arg Pro Ser Thr Pro Arg Ile Asp
 1 5 10 15

Arg Gly Ile Ala Leu His Lys Met Ile Arg Leu Val Thr Met Gly Leu
 20 25 30

Gly Gly Glu Gly Tyr Leu Asn Phe Met Gly Asn Glu Phe Gly His Pro
 35 40 45

Glu Trp Ile Asp Phe Pro Arg Gly Pro Gln Thr Leu Pro Thr Gly Lys
 50 55 60

Val Leu Pro Gly Asn Asn Asn Ser Tyr Asp Lys Cys Arg Arg Arg Phe
 65 70 75 80

Asp Leu Gly Asp Ala Asp Phe Leu Arg Tyr Arg Gly Met Gln Glu Phe
 85 90 95

Asp Gln Ala Met Gln His Leu Glu Glu Lys Tyr Gly Phe Met Thr Ser
 100 105 110

Glu His Gln Tyr Val Ser Arg Lys His Glu Glu Asp Lys Val Ile Ile
 115 120 125

Phe Glu Arg Gly Asp Leu Val Phe Val Phe Asn Phe His Trp Ser Asn
 130 135 140

Ser Phe Phe Asp Tyr Arg Val Gly Cys Ser Lys Pro Gly Lys Tyr Lys
 145 150 155 160

Val Ala Leu Asp Ser Asp Asp Ala Leu Phe Gly Gly Phe Ser Arg Leu

Val Ala Arg Ile Pro Asp Val Ser Met Glu Ser Glu Asp Ser Asn Leu
 725 730 735

Asp Arg Ile Glu Asp Asn Ser Glu Asp Ala Val Asp Ala Gly Ile Leu
 740 745 750

Lys Val Glu Arg Glu Val Val Gly Asp Asn
 755 760

<210> 26

<211> 984

<212> DNA

<213> Triticum aestivum

<400> 26

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atatgtatga ttcatggct ctggatagac cttcaactcc tcgcattgat cgtggcatag 60
cattacataa aatgatcagg cttgtcacca tgggttttagg tggcgaaggc tatcttaact 120
tcatgggaaa tgagtttggg catcctgaat ggatagattt tccaagaggc ccgcaaactc 180
ttccaaccgg caaagttctc cctggaaata acaatagtta tgataaatgc cgccgtagat 240
ttgatcttgg agatgcagat tttcttagat atcgtggtat gcaagagtcc gaccaggcaa 300
tgcagcatct tgaggaaaaa tatgggttta tgacatctga gcaccagtat gtttcacgga 360
aacatgagga agataagggtg atcatcttcg aaagaggaga tttggtattc gttttcaact 420
tccaccggag caatagcttt tttgactacc gtgttgggtg ttccaggcct ggggaagtaca 480
aggtggcctt agactccgac gatgcactct ttggtggatt cagcaggcct gatcatgatg 540
tcgactactt cacaaccgaa catccgcatg acaacaggcc gcgctctttc tcggtgtaca 600
ctccgagcag aactgcggtc gtgtatgcc ttacagagta agaaccagca gctgcttggt 660
acaaggcaaa gagagaactc cagagagctc gtggatcgtg agcgaagcga cgggcaacgg 720
cgcgaggctg ctctaagcgc catgactggg aggggatcgt gcctcttccc cagatgccag 780
gaggagcaga tggataggta gcttggttgg gagcgctcga aagaaaatgg acgggcctgg 840
gtgtttgtcg tgctgcacta cctcctcct atcttgcaca tccccggttg tctttgtaca 900
tataactaat aattgcccgt gcgctcaacg tgaacatata aatattctaa taataggtta 960
tcccgtgaaa aaaaaaaaaa aaaa 984

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<210> 27

<211> 977

<212> DNA

<213> Triticum aestivum

<400> 27

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atatgtatga ttcatggct ctggatagac cttcaactcc tcgcattgat cgtggcatag 60
cattacataa aatgatcagg cttgtcacca tgggttttagg tggcgaaggc tatcttaact 120
tcatgggaaa tgagtttggg catcctgaat ggatagattt tccaagaggc ccgcaaactc 180
ttccaaccgg caaagttctc cctggaaata acaatagtta tgataaatgc cgccgtagat 240
ttgatcttgg agatgcagat tttcttagat atcgtggtat gcaagagtcc gaccaggcaa 300
tgcagcatct tgaggaaaaa tatgggttta tgacatctga gcaccagtat gtttcacgga 360
aacatgagga agataagggtg atcatcttcg aaagaggaga tttggtattt gttttcaact 420

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165 170 175
 Asp His Asp Val Asp Tyr Phe Thr Thr Glu His Pro His Asp Asn Arg
 180 185 190
 Pro Arg Ser Phe Leu Val Tyr Thr Pro Ser Arg Thr Ala Val Val Tyr
 195 200 205
 Ala Leu Thr Glu
 210
 <210> 29
 <211> 212
 <212> PRT
 <213> Zea mays
 <400> 29
 Met Tyr Asp Phe Met Ala Leu Asp Arg Pro Ser Thr Pro Thr Ile Asp
 1 5 10 15
 Arg Gly Ile Ala Leu His Lys Met Ile Arg Leu Ile Thr Met Gly Leu
 20 25 30
 Gly Gly Glu Gly Tyr Leu Asn Phe Met Gly Asn Glu Phe Gly His Pro
 35 40 45
 Glu Trp Ile Asp Phe Pro Arg Gly Pro Gln Arg Leu Pro Ser Gly Lys
 50 55 60
 Phe Ile Pro Gly Asn Asn Asn Ser Tyr Asp Lys Cys Arg Arg Arg Phe
 65 70 75 80
 Asp Leu Gly Asp Ala Asp Tyr Leu Arg Tyr His Gly Met Gln Glu Phe
 85 90 95
 Asp Gln Ala Met Gln His Leu Glu Gln Lys Tyr Glu Phe Met Thr Ser
 100 105 110
 Asp His Gln Tyr Ile Ser Arg Lys His Glu Glu Asp Lys Val Ile Val
 115 120 125
 Phe Glu Lys Gly Asp Leu Val Phe Val Phe Asn Phe His Cys Asn Asn
 130 135 140
 Ser Tyr Phe Asp Tyr Arg Ile Gly Cys Arg Lys Pro Gly Val Tyr Lys
 145 150 155 160

54

Val Val Leu Asp Ser Asp Ala Gly Leu Phe Gly Gly Phe Ser Arg Ile
 165 170 175

His His Ala Ala Glu His Phe Thr Ala Asp Cys Ser His Asp Asn Arg
 180 185 190

Pro Tyr Ser Phe Ser Val Tyr Thr Pro Ser Arg Thr Cys Val Val Tyr
 195 - 200 205

Ala Pro Val Glu
 210

<210> 30

<211> 216

<212> PRT

<213> Zea mays

<400> 30

Met Tyr Asp Phe Met Ala Leu Asp Arg Pro Ser Thr Pro Arg Ile Asp
 1 5 10 15

Arg Gly Ile Ala Leu His Lys Met Ile Arg Leu Val Thr Met Gly Leu
 20 25 30

Gly Gly Glu Gly Tyr Leu Asn Phe Met Gly Asn Glu Phe Gly His Pro
 35 40 45

Glu Trp Ile Asp Phe Pro Arg Gly Pro Gln Ser Leu Pro Asn Gly Ser
 50 55 60

Val Ile Pro Gly Asn Asn Asn Ser Phe Asp Lys Cys Arg Arg Arg Phe
 65 70 75 80

Asp Leu Gly Asp Ala Asp Tyr Leu Arg Tyr Arg Gly Met Gln Glu Phe
 85 90 95

Asp Gln Ala Met Gln His Leu Glu Gly Lys Tyr Glu Phe Met Thr Ser
 100 105 110

Asp His Ser Tyr Phe Ser Arg Lys His Glu Glu Asp Lys Val Ile Ile
 115 120 125

Phe Glu Arg Gly Asp Leu Val Phe Val Phe Asn Phe His Trp Ser Asn
 130 135 140

Ser Tyr Phe Asp Tyr Arg Val Gly Cys Phe Lys Pro Gly Lys Tyr Lys
 145 150 155 160

Ile Val Leu Asp Ser Asp Asp Gly Leu Phe Gly Gly Phe Ser Arg Leu
 165 170 175

Asp His Asp Ala Glu Tyr Phe Thr Ala Asp Trp Pro His Asp Asn Arg
 180 185 190

Pro Cys Ser Phe Ser Val Tyr Ala Pro Ser Arg Thr Ala Val Val Tyr
 195 200 205

Ala Pro Ala Gly Ala Glu Asp Glu
 210 215

<210> 31
 <211> 217
 <212> DNA
 <213> Zea mays

<400> 31
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 ttccaaaacc ggcagatgca tgcatgcatg ctacaataag gttctgatac tttaatcgat 120
 gctggaaagc ccatgcatct cgctgcgttg tcctctctat atatataaga ccttcaaggt 180
 gtcaattaaa catagagttt tcgttttttcg ctttcct 217

<210> 32
 <211> 686
 <212> PRT
 <213> Triticum aestivum

<400> 32
 Met Leu Cys Leu Ser Ser Ser Leu Leu Pro Arg Pro Ser Ala Ala Ala
 1 5 10 15
 Asp Arg Pro Leu Pro Gly Ile Ile Ala Gly Gly Gly Gly Gly Lys Arg
 20 25 30
 Leu Ser Val Val Pro Ser Val Pro Phe Leu Leu Arg Trp Leu Trp Pro
 35 40 45
 Arg Lys Ala Lys Ser Lys Ser Phe Val Ser Val Thr Ala Arg Gly Asn
 50 55 60
 Lys Ile Ala Ala Thr Thr Gly Tyr Gly Ser Asp His Leu Pro Ile Tyr
 65 70 75 80
 Asp Leu Asp Leu Lys Leu Ala Glu Phe Lys Asp His Phe Asp Tyr Thr
 85 90 95

56

Arg Asn Arg Tyr Ile Glu Gln Lys His Leu Ile Glu Lys His Glu Gly
 100 105 110

Ser Leu Glu Glu Phe Ser Lys Gly Tyr Leu Lys Phe Gly Ile Asn Thr
 115 120 125

Glu His Gly Ala Ser Val Tyr Arg Glu Trp Ala Pro Ala Ala Glu Glu
 130 135 140

Ala Gln Leu Val Gly Asp Phe Asn Asn Trp Asn Gly Ser Gly His Lys
 145 150 155 160

Met Ala Lys Asp Asn Phe Gly Val Trp Ser Ile Arg Ile Ser His Val
 165 170 175

Asn Gly Lys Pro Ala Ile Pro His Asn Ser Lys Val Lys Phe Arg Phe
 180 185 190

Arg His His Gly Val Trp Val Glu Gln Ile Pro Ala Trp Ile Arg Tyr
 195 200 205

Ala Thr Val Thr Ala Ser Glu Ser Gly Ala Pro Tyr Asp Gly Leu His
 210 215 220

Trp Asp Pro Pro Ser Ser Glu Arg Tyr Val Phe Asn His Pro Arg Pro
 225 230 235 240

Pro Lys Pro Asp Val Pro Arg Ile Tyr Glu Ala His Val Gly Val Ser
 245 250 255

Gly Gly Lys Leu Glu Ala Gly Thr Tyr Arg Glu Phe Pro Asp Asn Val
 260 265 270

Leu Pro Cys Leu Arg Ala Thr Asn Tyr Asn Thr Val Gln Leu Met Gly
 275 280 285

Ile Met Glu His Ser Asp Ser Ala Ser Phe Gly Tyr His Val Thr Asn
 290 295 300

Phe Phe Ala Val Ser Ser Arg Ser Gly Thr Pro Glu Asp Leu Lys Tyr
 305 310 315 320

Leu Ile Asp Lys Ala His Ser Leu Gly Leu Arg Val Leu Met Asp Val
 325 330 335

Val His Ser His Ala Ser Asn Asn Val Ile Asp Gly Leu Asn Gly Tyr
 340 345 350

Asp Val Gly Gln Ser Ala His Glu Ser Tyr Phe Tyr Thr Gly Asp Lys
 355 360 365

Gly Tyr Asn Lys Met Trp Asn Gly Arg Met Phe Asn Tyr Ala Asn Trp
 370 375 380

Glu Val Leu Arg Phe Leu Leu Ser Asn Leu Arg Tyr Trp Met Asp Glu
 385 390 395 400

Phe Met Phe Asp Gly Phe Arg Phe Val Gly Val Thr Ser Met Leu Tyr
 405 410 415

Asn His Asn Gly Ile Asn Met Ser Phe Asn Gly Asn Tyr Lys Asp Tyr
 420 425 430

Ile Gly Leu Asp Thr Asn Val Asp Ala Phe Val Tyr Met Met Leu Ala
 435 440 445

Asn His Leu Met His Lys Leu Phe Pro Glu Ala Ile Val Val Ala Val
 450 455 460

Asp Val Ser Gly Met Pro Val Leu Cys Trp Pro Val Asp Glu Gly Gly
 465 470 475 480

Leu Gly Phe Asp Tyr Arg Gln Ala Met Thr Ile Pro Asp Arg Trp Ile
 485 490 495

Asp Tyr Leu Glu Asn Lys Gly Asp Gln Gln Trp Ser Met Ser Ser Val
 500 505 510

Ile Ser Gln Thr Leu Thr Asn Arg Arg Tyr Pro Glu Lys Phe Ile Ala
 515 520 525

Tyr Ala Glu Arg Gln Asn His Ser Ile Ile Gly Ser Lys Thr Met Ala
 530 535 540

Phe Leu Leu Met Glu Trp Glu Thr Tyr Ser Gly Met Ser Ala Met Asp
 545 550 555 560

Pro Asp Ser Pro Thr Ile Asp Arg Ala Ile Ala Leu Gln Lys Met Ile
 565 570 575

His Phe Ile Thr Met Ala Phe Gly Gly Asp Ser Tyr Leu Lys Phe Met
 580 585 590

Gly Asn Glu Tyr Met Asn Ala Phe Val Gln Ala Val Asp Thr Pro Ser
 595 600 605

Asp Lys Cys Ser Phe Leu Ser Ser Ser Asn Gln Thr Ala Ser His Met
 610 615 620

Asn Glu Glu Glu Lys Gly Ser Ala Leu Thr Lys Gly Tyr Thr His Leu
 625 630 635 640

Arg Ser Gly Cys Phe Asp Pro Ser Leu Pro Ser Thr Ser Ser Cys Ala
 645 650 655

Phe Leu Gly Pro Ser Asn Gln Ser Pro Phe Ser Lys Pro Phe Ile Gly
 660 665 670

Phe Pro Gly Cys Ile Phe Cys Cys Gly Leu Phe Lys Gly Glu
 675 680 685

<210> 33

<211> 830

<212> PRT

<213> Triticum aestivum

<400> 33

Met Leu Cys Leu Thr Ala Pro Ser Cys Ser Pro Ser Leu Pro Pro Arg
 1 5 10 15

Pro Ser Arg Pro Ala Ala Asp Arg Pro Gly Pro Gly Ile Ser Gly Gly
 20 25 30

Gly Asn Val Arg Leu Ser Ala Val Pro Ala Pro Ser Ser Leu Arg Trp
 35 40 45

Ser Trp Pro Arg Lys Ala Lys Ser Lys Phe Ser Val Pro Val Ser Ala
 50 55 60

Pro Arg Asp Tyr Thr Met Ala Thr Ala Glu Asp Gly Val Gly Asp Leu
 65 70 75 80

Pro Ile Tyr Asp Leu Asp Pro Lys Phe Ala Gly Phe Lys Glu His Phe
 85 90 95

Ser Tyr Arg Met Lys Lys Tyr Leu Asp Gln Lys His Ser Ile Glu Lys
 100 105 110

His Glu Gly Gly Leu Glu Glu Phe Ser Lys Gly Tyr Leu Lys Phe Gly
 115 120 125

Ile Asn Thr Glu Asn Asp Ala Thr Val Tyr Arg Glu Trp Ala Pro Ala

130	135	140
Ala Met Asp Ala Gln Leu Ile Gly Asp Phe Asn Asn Trp Asn Gly Ser		
145	150	155 160
Gly His Arg Met Thr Lys Asp Asn Tyr Gly Val Trp Ser Ile Arg Ile		
	165	170 175
Ser His Val Asn Gly Lys Pro Ala Ile Pro His Asn Ser Lys Val Lys		
	180	185 190
Phe Arg Phe His Arg Gly Asp Gly Leu Trp Val Asp Arg Val Pro Ala		
	195	200 205
Trp Ile Arg Tyr Ala Thr Phe Asp Ala Ser Lys Phe Gly Ala Pro Tyr		
	210	215 220
Asp Gly Val His Trp Asp Pro Pro Ser Gly Glu Arg Tyr Val Phe Lys		
	225	230 235 240
His Pro Arg Pro Arg Lys Pro Asp Ala Pro Arg Ile Tyr Glu Ala His		
	245	250 255
Val Gly Met Ser Gly Glu Lys Pro Glu Val Ser Thr Tyr Arg Glu Phe		
	260	265 270
Ala Asp Asn Val Leu Pro Arg Ile Lys Ala Asn Asn Tyr Asn Thr Val		
	275	280 285
Gln Leu Met Ala Ile Met Glu His Ser Tyr Tyr Ala Ser Phe Gly Tyr		
	290	295 300
His Val Thr Asn Phe Phe Ala Val Ser Ser Arg Ser Gly Thr Pro Glu		
	305	310 315 320
Asp Leu Lys Tyr Leu Val Asp Lys Ala His Ser Leu Gly Leu Arg Val		
	325	330 335
Leu Met Asp Val Val His Ser His Ala Ser Ser Asn Lys Thr Asp Gly		
	340	345 350
Leu Asn Gly Tyr Asp Val Gly Gln Asn Thr Gln Glu Ser Tyr Phe His		
	355	360 365
Thr Gly Glu Arg Gly Tyr His Lys Leu Trp Asp Ser Arg Leu Phe Asn		
	370	375 380
Tyr Ala Asn Trp Glu Val Leu Arg Phe Leu Leu Ser Asn Leu Arg Tyr		

60

385

390

395

400

Trp Met Asp Glu Phe Met Phe Asp Gly Phe Arg Phe Asp Gly Val Thr
 405 410 415

Ser Met Leu Tyr Asn His His Gly Ile Asn Met Ser Phe Ala Gly Ser
 420 425 430

Tyr Lys Glu Tyr Phe Gly Leu Asp Thr Asp Val Asp Ala Val Val Tyr
 435 440 445

Leu Met Leu Ala Asn His Leu Met His Lys Leu Leu Pro Glu Ala Thr
 450 455 460

Val Val Ala Glu Asp Val Ser Gly Met Pro Val Leu Cys Arg Ser Val
 465 470 475 480

Asp Glu Gly Gly Val Gly Phe Asp Tyr Arg Leu Ala Met Ala Ile Pro
 485 490 495

Asp Arg Trp Ile Asp Tyr Leu Lys Asn Lys Asp Asp Leu Glu Trp Ser
 500 505 510

Met Ser Gly Ile Ala His Thr Leu Thr Asn Arg Arg Tyr Thr Glu Lys
 515 520 525

Cys Ile Ala Tyr Ala Glu Ser His Asp Gln Ser Ile Val Gly Asp Lys
 530 535 540

Thr Met Ala Phe Leu Leu Met Asp Lys Glu Met Tyr Thr Gly Met Ser
 545 550 555 560

Asp Leu Gln Pro Ala Ser Pro Thr Ile Asp Arg Gly Ile Ala Leu Gln
 565 570 575

Lys Met Ile His Phe Ile Thr Met Ala Leu Gly Gly Asp Gly Tyr Leu
 580 585 590

Asn Phe Met Gly Asn Glu Phe Gly His Pro Glu Trp Ile Asp Phe Pro
 595 600 605

Arg Glu Gly Asn Asn Trp Ser Tyr Asp Lys Cys Arg Arg Gln Trp Ser
 610 615 620

Leu Ala Asp Ile Asp His Leu Arg Tyr Lys Tyr Met Asn Ala Phe Asp
 625 630 635 640

Gln Ala Met Asn Ala Leu Asp Asp Lys Phe Ser Phe Leu Ser Ser Ser

61

645

650

655

Lys Gln Ile Val Ser Asp Met Asn Glu Glu Lys Lys Ile Ile Val Phe
 660 665 670

Glu Arg Gly Asp Leu Val Phe Val Phe Asn Phe His Pro Ser Lys Thr
 675 680 685

Tyr Asp Gly Tyr Lys Val Gly Cys Asp Leu Pro Gly Lys Tyr Lys Val
 690 695 700

Ala Leu Asp Ser Asp Ala Leu Met Phe Gly Gly His Gly Arg Val Ala
 705 710 715 720

His Asp Asn Asp His Phe Thr Ser Pro Glu Gly Val Pro Gly Val Pro
 725 730 735

Glu Thr Asn Phe Asn Asn Arg Pro Asn Ser Phe Lys Ile Leu Ser Pro
 740 745 750

Ser Arg Thr Cys Val Ala Tyr Tyr Arg Val Glu Glu Lys Ala Glu Lys
 755 760 765

Pro Lys Asp Glu Gly Ala Ala Ser Trp Gly Lys Thr Ala Leu Gly Tyr
 770 775 780

Ile Asp Val Glu Ala Thr Gly Val Lys Asp Ala Ala Asp Gly Glu Ala
 785 790 795 800

Thr Ser Gly Ser Glu Lys Ala Ser Thr Gly Gly Asp Ser Ser Lys Lys
 805 810 815

Gly Ile Asn Phe Val Phe Leu Ser Pro Asp Lys Asp Asn Lys
 820 825 830

<210> 34

<211> 818

<212> PRT

<213> Triticum aestivum

<400> 34

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Gly Gly Val Asp Leu Pro Ser Leu Leu Leu Arg Lys Lys Asp Ser Ser
 35 40 45

Arg Ala Ala Ser Pro Gly Lys Val Leu Val Pro Asp Gly Glu Ser Asp
 50 55 60

Asp Leu Ala Ser Pro Ala Gln Pro Glu Glu Leu Gln Ile Pro Glu Asp
 65 70 75 80

Ile Glu Glu Gln Thr Ala Glu Val Asn Met Thr Gly Gly Thr Ala Glu
 85 90 95

Lys Leu Glu Ser Ser Glu Pro Thr Gln Gly Ile Val Glu Thr Ile Thr
 100 105 110

Asp Gly Val Thr Lys Gly Val Lys Glu Leu Val Val Gly Glu Lys Pro
 115 120 125

Arg Val Val Pro Lys Pro Gly Asp Gly Gln Lys Ile Tyr Glu Ile Asp
 130 135 140

Pro Thr Leu Lys Asp Phe Arg Ser His Leu Asp Tyr Arg Tyr Ser Glu
 145 150 155 160

Tyr Arg Arg Ile Arg Ala Ala Ile Asp Gln His Glu Gly Gly Leu Glu
 165 170 175

Ala Phe Ser Arg Gly Tyr Glu Lys Leu Gly Phe Thr Arg Ser Ala Glu
 180 185 190

Gly Ile Thr Tyr Arg Glu Trp Ala Pro Gly Ala His Ser Ala Ala Leu
 195 200 205

Val Gly Asp Phe Asn Asn Trp Asn Pro Asn Ala Asp Thr Met Thr Arg
 210 215 220

Asp Asp Tyr Gly Val Trp Glu Ile Phe Leu Pro Asn Asn Ala Asp Gly
 225 230 235 240

Ser Pro Ala Ile Pro His Gly Ser Arg Val Lys Ile Arg Met Asp Thr
 245 250 255

Pro Ser Gly Val Lys Asp Ser Ile Ser Ala Trp Ile Lys Phe Ser Val
 260 265 270

Gln Ala Pro Gly Glu Ile Pro Phe Asn Gly Ile Tyr Tyr Asp Pro Pro
 275 280 285

Glu Glu Glu Lys Tyr Val Phe Gln His Pro Gln Pro Lys Arg Pro Glu
 290 295 300

Ser Leu Arg Ile Tyr Glu Ser His Ile Gly Met Ser Ser Pro Glu Pro
 305 310 315 320

Lys Ile Asn Ser Tyr Ala Asn Phe Arg Asp Glu Val Leu Pro Arg Ile
 325 330 335

Lys Arg Leu Gly Tyr Asn Ala Val Gln Ile Met Ala Ile Gln Glu His
 340 345 350

Ser Tyr Tyr Ala Ser Phe Gly Tyr His Val Thr Asn Phe Phe Ala Pro
 355 360 365

Ser Ser Arg Phe Gly Thr Pro Glu Asp Leu Lys Ser Leu Ile Asp Arg
 370 375 380

Ala His Glu Leu Gly Leu Ile Val Leu Met Asp Ile Val His Ser His
 385 390 395 400

Ser Ser Asn Asn Thr Leu Asp Gly Leu Asn Gly Phe Asp Gly Thr Asp
 405 410 415

Thr His Tyr Phe His Gly Gly Pro Arg Gly His His Trp Met Trp Asp
 420 425 430

Ser Arg Leu Phe Asn Tyr Gly Ser Trp Glu Val Leu Arg Phe Leu Leu
 435 440 445

Ser Asn Ala Arg Trp Trp Leu Glu Glu Tyr Lys Phe Asp Gly Phe Arg
 450 455 460

Phe Asp Gly Val Thr Ser Met Met Tyr Thr His His Gly Leu Gln Met
 465 470 475 480

Thr Phe Thr Gly Asn Tyr Gly Glu Tyr Phe Gly Phe Ala Thr Asp Val
 485 490 495

Asp Ala Val Val Tyr Leu Met Leu Val Asn Asp Leu Ile His Gly Leu
 500 505 510

His Pro Asp Ala Val Ser Ile Gly Glu Asp Val Ser Gly Met Pro Thr
 515 520 525

Phe Cys Ile Pro Val Pro Asp Gly Gly Val Gly Leu Asp Tyr Arg Leu
 530 535 540

His Met Ala Val Ala Asp Lys Trp Ile Glu Leu Leu Lys Gln Ser Asp
 545 550 555 560

Glu Ser Trp Lys Met Gly Asp Ile Val His Thr Leu Thr Asn Arg Arg
 565 570 575

Trp Leu Glu Lys Cys Val Thr Tyr Ala Glu Ser His Asp Gln Ala Leu
 580 585 590

Val Gly Asp Lys Thr Ile Ala Phe Trp Leu Met Asp Lys Asp Met Tyr
 595 600 605

Asp Phe Met Ala Leu Asp Arg Pro Ser Thr Pro Arg Ile Asp Arg Gly
 610 615 620

Ile Ala Leu His Lys Met Ile Arg Leu Val Thr Met Gly Leu Gly Gly
 625 630 635 640

Glu Gly Tyr Leu Asn Phe Met Gly Asn Glu Phe Gly His Pro Glu Trp
 645 650 655

Ile Asp Phe Pro Arg Gly Pro Gln Thr Leu Pro Thr Gly Lys Val Leu
 660 665 670

Pro Gly Asn Asn Asn Ser Tyr Asp Lys Cys Arg Arg Arg Phe Asp Leu
 675 680 685

Gly Asp Ala Asp Phe Leu Arg Tyr His Gly Met Gln Glu Phe Asp Gln
 690 695 700

Ala Met Gln His Leu Glu Glu Lys Tyr Gly Phe Met Thr Ser Glu His
 705 710 715 720

Gln Tyr Val Ser Arg Lys His Glu Glu Asp Lys Val Ile Ile Phe Glu
 725 730 735

Arg Gly Asp Leu Val Phe Val Phe Asn Phe His Trp Ser Asn Ser Phe
 740 745 750

Phe Asp Tyr Arg Val Gly Cys Ser Arg Pro Gly Lys Tyr Lys Val Ala
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Leu Asp Ser Asp Asp Ala Leu Phe Gly Gly Phe Ser Arg Leu Asp His
 770 775 780

Asp Val Asp Tyr Phe Thr Thr Glu His Pro His Asp Asn Arg Pro Arg
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65

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805 810 815

Thr Glu

<210> 35

<211> 813

<212> DNA

<213> Escherichia coli

<400> 35

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<210> 36

<211> 7

<212> PRT

<213> Triticum aestivum

<400> 36

Met Asp Lys Asp Met Tyr Asp

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5

<210> 37

<211> 40

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: synthetic
oligonucleotide

<400> 37

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<210> 38

<211> 17

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:synthetic
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<400> 38

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17

<210> 39

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:synthetic
oligonucleotide

<400> 39

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20

<210> 40

<211> 21

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence:synthetic
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<400> 40

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21

<210> 41

<211> 21

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence:synthetic
oligonucleotide

<400> 41
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21

<210> 42
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<212> PRT
<213> Triticum aestivum

<400> 42
Gly Val Trp Glu Ile Phe Leu Pro
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<210> 43
<211> 10
<212> DNA
<213> Artificial Sequence

<220>
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oligonucleotide

<400> 43
cgggatcccg

10

<210> 44
<211> 34
<212> DNA
<213> Artificial Sequence

<220>
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<400> 44
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34

<210> 45
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:synthetic
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<400> 45
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30

<210> 46
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<212> DNA
<213> Artificial Sequence

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<223> Description of Artificial Sequence:synthetic
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27

<210> 47
<211> 35
<212> DNA
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oligonucleotide

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35

<210> 48
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:synthetic
oligonucleotide

<400> 48
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30

<210> 49
<211> 30
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<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:synthetic
oligonucleotide

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30

<210> 50

<211> 21

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence:synthetic
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<400> 50

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21

<210> 51

<211> 21

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence:synthetic
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21

<210> 52

<211> 2037

<212> DNA

<213> Zea mays

<400> 52

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<210> 53

<211> 1085

<212> DNA

<213> Triticum aestivum

<400> 53

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<212> PRT

<213> Triticum aestivum

<400> 54

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 35 40 45

Lys Ala Lys Ser Lys Ser Ser Val Pro Val Xaa Ala Xaa Xaa Xaa Xaa
 50 55 60

Ile Xaa Ala Thr Xaa Xaa Xaa Gly Val Xaa Xaa Leu Pro Ile Tyr Asp
 65 70 75 80

Leu Asp Pro Lys Leu Ala Xaa Phe Lys Xaa His Phe Asp Tyr Arg Xaa
 85 90 95

Xaa Xaa Tyr Xaa Xaa Gln Lys His Xaa Ile Glu Lys His Glu Gly Gly
 100 105 110

Leu Glu Glu Phe Ser Lys Gly Tyr Leu Lys Phe Gly Ile Asn Thr Glu
 115 120 125

Xaa Xaa Ala Xaa Val Tyr Arg Glu Trp Ala Pro Ala Ala Xaa Xaa Ala
 130 135 140

Gln Leu Val Gly Asp Phe Asn Asn Trp Asn Gly Ser Gly His Xaa Met
 145 150 155 160

Thr Lys Asp Asn Phe Gly Val Trp Ser Ile Arg Leu Ser Asn Asn Ala
 165 170 175

Asp Gly Ser Pro Ala Ile Pro His Gly Ser Lys Val Lys Phe Arg Phe
 180 185 190

Asp Thr Pro Ser Gly Val Trp Val Asp Ser Ile Pro Ala Trp Ile Lys
 195 200 205

Tyr Ala Val Gln Thr Ala Gly Glu Ile Gly Ala Pro Tyr Asp Gly Ile
 210 215 220

His Tyr Asp Pro Pro Ser Glu Glu Lys Tyr Val Phe Lys His Pro Gln
 225 230 235 240

Pro Lys Lys Pro Asp Ser Leu Arg Ile Tyr Glu Ala His Val Gly Met

72

245

250

255

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Val Leu Pro Arg Ile Lys Ala Leu Gly Tyr Asn Ala Val Gln Leu Met
 275 280 285

Ala Ile Gln Glu His Ser Tyr Tyr Ala Ser Phe Gly Tyr His Val Thr
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Asn Phe Phe Ala Val Ser Ser Arg Ser Gly Thr Pro Glu Asp Leu Lys
 305 310 315 320

Ser Leu Ile Asp Lys Ala His Ser Leu Gly Leu Arg Val Leu Met Asp
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Val Val His Ser His Ala Ser Asn Asn Thr Leu Asp Gly Leu Asn Gly
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Glu Phe Lys Phe Asp Gly Phe Arg Phe Asp Gly Val Thr Ser Met Leu
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Tyr Thr His His Gly Leu Asn Met Ser Phe Thr Gly Ser Tyr Lys Glu
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Tyr Phe Gly Leu Ala Thr Asp Val Asp Ala Val Val Tyr Leu Met Leu
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Ala Asn Asp Leu Ile His Gly Leu Xaa Pro Glu Ala Val Val Val Gly
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Glu Asp Val Ser Gly Met Pro Val Leu Cys Xaa Pro Val Asp Glu Gly
 465 470 475 480

Gly Val Gly Phe Asp Tyr Arg Leu Ala Met Ala Val Ala Asp Lys Trp
 485 490 495

Ile Asp Leu Leu Lys Asn Lys Asp Asp Xaa Trp Ser Met Gly Xaa Ile

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505

510

Val His Thr Leu Thr Asn Arg Arg Tyr Pro Glu Lys Cys Val Ala Tyr
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Ala Glu Ser His Asp Gln Ala Leu Val Gly Asp Lys Thr Ile Ala Phe
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Ser Ser Pro Thr Ile Asp Arg Gly Ile Ala Leu Gln Lys Met Ile His
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Leu Ile Thr Met Gly Leu Gly Gly Asp Gly Tyr Leu Asn Phe Met Gly
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Asn Glu Phe Gly His Pro Glu Trp Ile Asp Phe Pro Arg Gly Pro Gln
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Leu Pro Thr Gly Lys Pro Gly Asn Asn Asn Ser Tyr Asp Lys Cys Arg
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Asn Ala Phe Asp Gln Ala Met Gln His Leu Glu Asp Lys Tyr Gly Phe
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Leu Ser Ser Ser His Gln Tyr Val Ser Arg Lys Asn Glu Glu Asp Lys
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Val Ile Val Phe Glu Lys Gly Asp Leu Val Phe Val Phe Asn Phe His
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Trp Ser Asn Ser Tyr Phe Asp Tyr Arg Val Gly Cys Xaa Xaa Pro Gly
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Gly Arg Xaa Xaa His Asp Xaa Asp His Phe Thr Ser Glu Xaa Xaa His
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Asp Asn Arg Pro Xaa Ser Phe Ser Val Leu Thr Pro Ser Arg Thr Cys
 740 745 750

Val Val Tyr Ala Pro Xaa Glu Xaa Ala Ala Xaa Val Thr Lys Xaa Tyr

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770				775				780							
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<211> 1488
<212> DNA
<213> Zea mays
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<400> 55

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INTERNATIONAL SEARCH REPORT

International Application No
PCT/GB 99/03011

A. CLASSIFICATION OF SUBJECT MATTER

IPC 7 C12N15/82 C12N9/10 A23L1/0522 A01H5/00

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

IPC 7 C12N A23L A01H

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the International search (name of data base and, where practical, search terms used)

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	WO 97 22703 A (DU PONT ; HUBBARD NATALIE LOUISE (US); KLEIN THEODORE MITCHELL (US)) 26 June 1997 (1997-06-26) cited in the application	1-4, 6-15, 17-25
Y	see the claims see SEQ ID NO: 1 (page 50-53) abstract; figures 1,2,6-15; examples 1-3,7 page 1 -page 7 page 14, line 29 -page 21, line 35 -/-	14-25

☒ Further documents are listed in the continuation of box C.

☒ Patent family members are listed in annex.

* Special categories of cited documents:

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Date of the actual completion of the international search

20 December 1999

Date of mailing of the international search report

11/01/2000

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Oderwald, H

INTERNATIONAL SEARCH REPORT

Inter. Application No
PCT/GB 99/03011

C. (Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	NAIR R B ET AL: "Isolation, characterization and expression analysis of a starch branching enzyme II cDNA from wheat" PLANT SCIENCE, vol. 122, 1997, pages 153-163, XP002095263 cited in the application	5, 7, 9-14, 16-25
Y	abstract; figures 2-5 page 154 -page 156 page 159 page 162	15
X	SUN C. ET AL.: "The two genes encoding starch-branching enzymes IIa and IIb are differentially expressed in barley" PLANT PHYSIOLOGY, vol. 118, 1 September 1998 (1998-09-01), pages 37-49, XP002095264	1-13
Y	abstract; figures 1-3 page 45, paragraph 7 -page 47, paragraph 2	14-25
P, X	WO 99 14314 A (GOODMAN FIELDER LTD ;LI ZHONGYI (AU); MORELL MATTHEW (AU); RAHMAN) 25 March 1999 (1999-03-25) abstract; claims 1-52 see SEQ ID NO: 10 and 12 (pp.75-81 and 83-85) page 6 -page 10	5-7, 9-25

INTERNATIONAL SEARCH REPORT

International application No.

PCT/GB 99/03011

Box I Observations where certain claims were found unsearchable (Continuation of item 1 of first sheet)

This International Search Report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☐ Claims Nos.:
because they relate to subject matter not required to be searched by this Authority, namely:
2. ☐ Claims Nos.:
because they relate to parts of the International Application that do not comply with the prescribed requirements to such an extent that no meaningful International Search can be carried out, specifically:
3. ☐ Claims Nos.:
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

Box II Observations where unity of invention is lacking (Continuation of item 2 of first sheet)

This International Searching Authority found multiple inventions in this International application, as follows:

See additional sheet

1. ☐ As all required additional search fees were timely paid by the applicant, this International Search Report covers all searchable claims.
2. ☒ As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.
3. ☐ As only some of the required additional search fees were timely paid by the applicant, this International Search Report covers only those claims for which fees were paid, specifically claims Nos.:
4. ☐ No required additional search fees were timely paid by the applicant. Consequently, this International Search Report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:

Remark on Protest

- ☐ The additional search fees were accompanied by the applicant's protest.
- ☐ No protest accompanied the payment of additional search fees.

INTERNATIONAL SEARCH REPORT

International Application No. PCT/ GB 99/03011

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

This International Searching Authority found multiple (groups of) inventions in this international application, as follows:

1. Claims: 1-4, 6, 8, all complete; 7, 9-25 all partially

Nucleotide sequence encoding wheat SBEII-1 members 5A1, B2, B4, B10 or B6 3' UTR sequences thereof, vectors, host cells, amino acid sequences encoded by said nucleotide plant; plants and parts thereof, starch, a method for making altered starch, use of that starch, foodstuff containing said nucleotide sequences.

2. Claims: 5 complete; 7, 9-25 partially

Nucleotide sequence encoding wheat SBEII-2 member B1. Vectors, host cells, amino acid sequence encoded by said nucleotide sequence. Methods for altering the characteristics of a plant; plants and parts thereof starch, a method for making altered starch, use of that starch, foodstuff containing said starch using said nucleotide sequence.

INTERNATIONAL SEARCH REPORT

information on patent family members

Inter national Application No

PCT/GB 99/03011

Patent document cited in search report	Publication date	Patent family member(s)	Publication date
W0 9722703 A	26-06-1997	AU 1684697 A	14-07-1997
		BR 9612086 A	17-02-1999
		CA 2239979 A	26-06-1997
		CN 1219199 A	09-06-1999
		EP 0868520 A	07-10-1998
		HU 9902112 A	28-10-1999
W0 9914314 A	25-03-1999	AU 8967098 A	05-04-1999

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